

Tue Dec 10 10:51:32 2002

us-09-880-457-1_COPY_486_746.rml

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:19 : Search time 15.2491 Seconds
(without alignments)
5249.015 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atgcaatccctgacgctcag.....gtaattgagaatcattcac 261

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA.*

- 1: /cgn2_6/prodata/1/lna/5A.COMB.seq.*
- 2: /cgn2_6/prodata/1/lna/5B.COMB.seq.*
- 3: /cgn2_6/prodata/1/lna/6A.COMB.seq.*
- 4: /cgn2_6/prodata/1/lna/6B.COMB.seq.*
- 5: /cgn2_6/prodata/1/lna/PCITUS.COMB.seq.*
- 6: /cgn2_6/prodata/1/lna/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121.2	46.4	954	US-08-996-139-12	Sequence 12, Appl
2	121.2	46.4	954	US-08-995-659-12	Sequence 12, Appl
3	121.2	46.4	954	US-09-215-649A-12	Sequence 12, Appl
4	121.2	46.4	954	US-09-577-780-12	Sequence 3, Appl
5	121.2	46.4	2271	US-09-052-521C-3	Sequence 10, Appl
6	95.6	36.6	1630	US-08-996-139-10	Sequence 10, Appl
7	95.6	36.6	1630	US-08-995-659-10	Sequence 10, Appl
8	95.6	36.6	1630	US-09-215-649A-10	Sequence 10, Appl
9	95.6	36.6	1630	US-09-577-780-10	Sequence 10, Appl
10	95.6	36.6	2191	US-08-989-362-1	Sequence 6, Appl
11	95.6	36.6	2295	US-08-842-842-6	Sequence 1, Appl
12	95.6	36.6	2295	US-09-052-521C-1	Sequence 22, Appl
13	95.6	36.6	2295	US-09-003-574-22	Sequence 22, Appl
14	95.6	36.6	2295	US-09-003-574-22	Sequence 20, Appl
15	95.6	36.6	2295	US-09-003-574-20	Sequence 20, Appl
16	95.6	36.6	2295	US-09-003-574-20	Sequence 21, Appl
17	95.6	36.6	2295	US-09-003-574-21	Sequence 21, Appl
18	95.6	36.6	2295	US-09-003-574-21	Sequence 1, Appl
19	95.6	36.6	2295	US-08-463-262A-1	Sequence 1, Appl
20	95.6	36.6	2295	US-08-463-262A-1	Sequence 1, Appl
21	95.6	36.6	2295	US-09-003-574-1	Sequence 1, Appl
22	95.6	36.6	2295	US-09-003-574-1	Sequence 33, Appl
23	95.6	36.6	2295	US-09-003-574-33	Sequence 32, Appl
24	95.6	36.6	2295	US-09-003-574-32	Sequence 32, Appl
25	95.6	36.6	2295	US-09-003-574-32	Sequence 30, Appl
26	95.6	36.6	2295	US-09-003-574-30	Sequence 30, Appl
27	95.6	36.6	2295	US-09-003-574-30	Sequence 30, Appl

28	29.8	11.4	2076	4	US-09-003-570-30	Sequence 30, Appl
29	29.8	11.4	2126	1	US-08-463-262A-2	Sequence 2, Appl
30	29.8	11.4	2126	1	US-08-463-989-2	Sequence 2, Appl
31	29.8	11.4	2126	4	US-09-003-574-2	Sequence 2, Appl
32	29.8	11.4	2126	4	US-09-003-570-2	Sequence 29, Appl
33	29.8	11.4	2292	4	US-09-003-574-29	Sequence 29, Appl
34	29.8	11.4	2292	4	US-09-003-570-29	Sequence 47, Appl
35	29.4	11.3	1461	1	US-07-968-971A-5	Sequence 7, Appl
36	29.4	11.3	1461	1	US-07-824-247-47	Sequence 9, Appl
37	29.4	11.3	1461	1	US-08-143-473A-7	Sequence 7, Appl
38	29.4	11.3	1461	1	US-08-463-523B-9	Sequence 7, Appl
39	29.4	11.3	1461	1	US-08-469-203A-7	Sequence 7, Appl
40	29.4	11.3	1461	3	US-08-470-204A-7	Sequence 47, Appl
41	29.4	11.3	1461	3	US-08-926-522-12	Sequence 12, Appl
42	29.4	11.3	1461	4	US-08-926-522-12	Sequence 21, Appl
43	29.4	11.3	804	4	US-09-003-574-21	Sequence 21, Appl
44	29.4	11.3	804	4	US-09-003-570-21	Sequence 1, Appl
45	29.4	11.3	1299	1	US-08-463-262A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION NUMBER: US/08/996,139
APPLICATION NUMBER: 1997
FILING DATE: 22 DECEMBER 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
FILING DATE: 12 DECEMBER 1997

SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 1..951
US-08-996-139-12

Query Match 46.4%; Score 121.2; DB 3; Length 954;
Best Local Similarity 74.8%; Pred. No. 1.3e-34;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCTGACGCTGACGCTTCACTCATCTGTTATATACATCAATATCCATGAG 63
DB 473 GCAAGCTTGAAGCTGACGCTTTGCTCATCTCATTTATATGCAACGACATCCATCTG 532
QY 64 GCT--CATAAAGAGATCTTTCTTCTGAAACATGACCAAGATTGGGCAAGCTTCCA 121
DB 533 GTTCCCATTAAGTGTCTGTCTCTGTAACATGATCGGGGTTGGGCCAAGATCTCCA 592
QY 122 ACATGACTTTCAGCAGGAAAGAACTAAGTCA-----AAGCATTTATTTACCGGAATG 175
DB 593 ACATGACTTTTACGAAATGAAACTATATAGTATATGAGATGCTTTTATTTACCTGTATG 652
QY 176 CCGACATTTGCTCTGACATCGGTTAACCCTGACAGCCTTAACCTGACAGCCTTGAGC 235
DB 653 CCAACATTTGCTTTGACATCATGAAACTTTCAGAGACCTTACAGATATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 2

US-08-995-659-12
Sequence 12, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:

FEATURE: hURANKL (full length)
NAME/KEY: CDS
LOCATION: 1..951
US-08-995-659-12

Query Match

Best Local Similarity 74.8%; Pred. No. 1.3e-34;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCTGACGCTGACGCTTCACTCATCTGTTATATACATCAATATCCATGAG 63
DB 473 GCAAGCTTGAAGCTGACGCTTTGCTCATCTCATTTATATGCAACGACATCCATCTG 532
QY 64 GCT--CATAAAGAGATCTTTCTTCTGAAACATGACCAAGATTGGGCAAGCTTCCA 121
DB 533 GTTCCCATTAAGTGTCTGTCTCTGTAACATGATCGGGGTTGGGCCAAGATCTCCA 592
QY 122 ACATGACTTTCAGCAGGAAAGAACTAAGTCA-----AAGCATTTATTTACCGGAATG 175
DB 593 ACATGACTTTTACGAAATGAAACTATATAGTATATGAGATGCTTTTATTTACCTGTATG 652
QY 176 CCGACATTTGCTCTGACATCGGTTAACCCTGACAGCCTTAACCTGACAGCCTTGAGC 235
DB 653 CCAACATTTGCTTTGACATCATGAAACTTTCAGAGACCTTACAGATATCTTCAAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 3

US-09-215-649A-12
Sequence 12, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

पञ्च

TITLE OF INVENTION: Ligand for metal

236 TA 237

236 TA 237

Tue Dec 10 10:51:32 2002

us-09-880-457-1_copy_486_746.rni

APPLICANT: Maraskovsky, Eugene
 TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/995,659
 FILING DATE: 22 DECEMBER 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 60/064,671
 FILING DATE: 14 OCTOBER 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2852-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1630 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 IMMEDIATE SOURCE:
 LIBRARY: RANKL
 CLONE: RANKL
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..884
 US-08-995-659-10
 Query Match 36.6%; Score 95.6; DB 4; Length 1630;
 Best Local Similarity 68.2%; Pred. No. 4.2e-25;
 Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps 2;

QY 3 GGCATCTGAGCGCTTCATCTTGTATTAATACCAATATCCATGA 62
 DB 405 GGCATCTGAGCGCTTCATCTTGTATTAATACCAATATCCATGA 62
 QY 63 GG--CTCATTAACGAGCTTTCTTGTGAAACATGACCAAGATTGGCAACGCTCC 120
 DB 465 GGTTCCTTAAGTCACTCTCTCTTGTGTAACAGATCGAGGCTGGCAAGATCTCT 524
 QY 121 AACATGACTTTCAGCAAGCAAACTAAGATCA-----AAGCATTTATTACCGGAAT 174
 DB 525 AACATGACTTTCAGCAAGCAAACTAAGATCA-----AAGCATTTATTACCGGAAT 174

QY 175 GCGACATTTGCTCTGCATCGCGTAACTCAGCAGGCTTACTCTGAGACCTTCAG 234
 DB 585 GCGACATTTGCTCTGCATCGCGTAACTCAGCAGGCTTACTCTGAGACCTTCAG 234
 QY 235 CT 236
 DB 645 CT 646
 RESULT 8
 US-09-215-649A-10
 Sequence 10, Application US/09215649A
 Patent No. 6271349
 GENERAL INFORMATION:
 APPLICANT: Anderson, Dirk M.
 Maraskovsky, Eugene
 Galibert, Laurent
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/215,649A
 FILING DATE: 17-Dec-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/996,139
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1630 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 IMMEDIATE SOURCE:
 LIBRARY: <Unknown>
 CLONE: RANKL
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..884
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-215-649A-10
 Query Match 36.6%; Score 95.6; DB 4; Length 1630;
 Best Local Similarity 68.2%; Pred. No. 4.2e-25;
 Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps 2;

QY 3 GGCAATCTGAGCGCTGAGCCTTCAACATCTTTATTATACATCATATATCCATGA 62
Db 405 GGCAAGCCTGAGGCCAGGCTGATTCGACACCTCAACATCATGCTGCACATCCATCG 464
QY 63 GG--CTCATTAAGAGAGATCTTTCTTTGGAACATACCAAGATTTGGGCAAGCTTCC 120
Db 465 GGTTCCTCATTAAGATCTGCTCTCTTGGTACCATGAGGCTGCGCAAGATCTCT 524
QY 121 AACATGACTTTGACGCAAGCAAGAACTAAGTCA-----AAGCATTTATTACCGGAT 174
Db 525 AACATGAGCTTAAGCAAGCAAGAACTAAGGTTAAACCAAGATGCTTCTATTACCTGAC 584
QY 175 GCGCAGATTTGCTCTGACATCGCGTAACCTGACGAGGCTTACCTGACGAGCTTAC 234
Db 585 GCGAAGCTTTGCTTGGCATCATGAACATCGGAGACGCTTACGAGACTATCTTACG 644
QY 235 CT 236
Db 645 CT 646

RESULT 9

US-09-577-780-10

Sequence 10, Application US/09577780
Patent No. 6419929

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Power Macintosh

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/577,780

FILING DATE: 24-May-2000

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: <unknown>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mus musculus

IMMEDIATE SOURCE:

LIBRARY: <unknown>
CLONE: RANKL

FEATURE:

NAME/KEY: CDS

LOCATION: 3..884

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-577-780-10

Query Match

Best Local Similarity 36.6%; Score 95.6; DB 4; Length 1630;

Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps 2;

QY 3 GGCAATCTGAGCGCTGAGCCTTCAACATCTTTATTATACATCATATATCCATGA 62
Db 405 GGCAAGCCTGAGGCCAGGCTGATTCGACACCTCAACATCATGCTGCACATCCATCG 464
QY 63 GG--CTCATTAAGAGAGATCTTTCTTTGGAACATACCAAGATTTGGGCAAGCTTCC 120
Db 465 GGTTCCTCATTAAGATCTGCTCTCTTGGTACCATGAGGCTGCGCAAGATCTCT 524
QY 121 AACATGACTTTGACGCAAGCAAGAACTAAGTCA-----AAGCATTTATTACCGGAT 174
Db 525 AACATGAGCTTAAGCAAGCAAGAACTAAGGTTAAACCAAGATGCTTCTATTACCTGAC 584
QY 175 GCGCAGATTTGCTCTGACATCGCGTAACCTGACGAGGCTTACCTGACGAGCTTAC 234
Db 585 GCGAAGCTTTGCTTGGCATCATGAACATCGGAGACGCTTACGAGACTATCTTACG 644
QY 235 CT 236
Db 645 CT 646

RESULT 10

US-08-989-362-1

Sequence 1, Application US/08989362
Patent No. 6242586

GENERAL INFORMATION:

APPLICANT: Gorman, Daniel M.

TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: DNA Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,362

FILING DATE: 12-DEC-1997

CLASSIFICATION: 56

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,846

FILING DATE: 13-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0686

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)496-1204

TELEFAX: (650)496-1204

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2191 base pairs

TYPE: nucleic acid

36.68; Score 95.6; DB 2; Length 2295;

RESULT 13

US-09-003-574-22

Sequence 22, Application US/09003574

Patent No. 6265198

GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia Ann

APPLICANT: Frank, Glenn R.

APPLICANT: Grieve, Robert B.

TITLE OF INVENTION: NOVEL PARASITE ASTACIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESSES:

ADDRESS: SHERIDAN ROSS P.C.

STREET: 1700 LINCOLN ST., SUITE 3500

CITY: DENVER

STATE: CO

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,574

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-21-1-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 271 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-003-574-22

Query Match

Best Local Similarity 11.4%; Score 29.8; DB 4; Length 271;

Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db

26 AACGATCTGTATTATACCATCATATCCATGAGGCTCATAAACGAGCTTT 82

70 AAATCATATTTTATTATATACCAATATTCATCAAGCGTTGGAACATTTTT 126

RESULT 14

US-09-003-570-22

Sequence 22, Application US/09003570

Patent No. 6281345

GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia Ann

APPLICANT: Frank, Glenn R.

APPLICANT: Grieve, Robert B.

TITLE OF INVENTION: NOVEL PARASITE ASTACIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESSES:

ADDRESS: SHERIDAN ROSS P.C.

STREET: 1700 LINCOLN ST., SUITE 3500

CITY: DENVER

STATE: CO

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,570

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-21-4-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 271 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-003-570-22

Query Match

Best Local Similarity 11.4%; Score 29.8; DB 4; Length 271;

Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db

26 AACGATCTGTATTATACCATCATATCCATGAGGCTCATAAACGAGCTTT 82

70 AAATCATATTTTATTATATACCAATATTCATCAAGCGTTGGAACATTTTT 126

RESULT 15

US-09-003-574-20

Sequence 20, Application US/09003574

Patent No. 6265198

GENERAL INFORMATION:

APPLICANT: Tripp, Cynthia Ann

APPLICANT: Frank, Glenn R.

APPLICANT: Grieve, Robert B.

TITLE OF INVENTION: NOVEL PARASITE ASTACIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESSES:

ADDRESS: SHERIDAN ROSS P.C.

STREET: 1700 LINCOLN ST., SUITE 3500

CITY: DENVER

STATE: CO

COUNTRY: USA

ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/003,574

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-21-1-C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 689 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

Tue Dec 10 10:51:32 2002

us-09-880-457-1_copy_486_746.rni

US-09-003-574-20

Query Match 11.4%; Score 29.8; DB 4; Length 689;
 Best Local Similarity 70.2%; Pred. No. 0.34; 17; Indels 0; Gaps 0;
 Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 Oy 26 AACTCATCTTGTATTAATACATCAATATTCATGAGCTCATTAACGAGCTTT 82
 60 AAATCAATATTTTATTAATTAACAACAATATTCATCAAGCCGTTGGAACAATTTT 116

Search completed: December 8, 2002, 17:28:26
 Job time : 22.2491 secs

11

Tue Dec 10 19:51:27 2002

us-09-880-457-1.rn1

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 8, 2002, 15:56:19 : Search time 67.8321 Seconds
(without alignments)
5249.015 Million cell updates/sec

Title: US-09-880-457-1
Perfect score: 1161
Sequence: 1 aaagaggaataatcaaga.....taataaagaggaataatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5b_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6a_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6b_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCPUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	126	10.9	954	3	US-08-996-139-12 Sequence 12, Appl
2	126	10.9	954	4	US-08-995-659-12 Sequence 12, Appl
3	126	10.9	954	4	US-09-215-649A-12 Sequence 12, Appl
4	126	10.9	954	4	US-09-577-780-12 Sequence 3, Appl
5	126	10.9	2271	4	US-09-052-521C-3 Sequence 10, Appl
6	97	8.4	1630	3	US-08-996-139-10 Sequence 10, Appl
7	97	8.4	1630	4	US-08-995-659-10 Sequence 10, Appl
8	97	8.4	1630	4	US-09-215-649A-10 Sequence 10, Appl
9	97	8.4	1630	4	US-09-577-780-10 Sequence 1, Appl
10	97	8.4	1291	4	US-08-989-362-1 Sequence 6, Appl
11	97	8.4	2293	2	US-08-842-842-6 Sequence 1, Appl
12	97	8.4	2293	2	US-08-052-521C-1 Sequence 14, Appl
13	53	4.6	7218	1	US-08-232-463-14 Sequence 17, Appl
14	37	3.2	289	4	US-09-007-005-17 Sequence 11, Appl
15	37	3.2	289	4	US-09-244-796-17 Sequence 10, Appl
16	37	3.2	99500	4	US-09-198-096-10 Sequence 1, Appl
17	34.6	3.0	68750	3	US-09-335-409-1 Sequence 1, Appl
18	34.6	3.0	68750	4	US-09-568-102-1 Sequence 1, Appl
19	34.6	3.0	68750	4	US-09-567-969-1 Sequence 1, Appl
20	34.6	3.0	68750	4	US-09-568-480-1 Sequence 1, Appl
21	34.6	3.0	68750	4	US-09-568-486-1 Sequence 1, Appl
22	34.6	3.0	68750	4	US-09-568-472-1 Sequence 1, Appl
23	34.6	3.0	68750	4	US-09-567-899-1 Sequence 1, Appl
24	34.6	3.0	68750	4	US-09-567-899-1 Sequence 3, Appl
25	33.8	2.9	1280	1	US-08-027-986-3 Sequence 4, Appl
26	33.8	2.9	2540	1	US-08-027-986-4 Sequence 1, Appl
27	33.8	2.9	1356	4	US-08-952-736A-1 Sequence 2, Appl

28	33.6	2.9	71989	4	US-09-443-501A-2 Sequence 2, Appl
29	32.8	2.8	2040	1	US-08-599-252-103 Sequence 103, App
30	32.8	2.8	2040	5	PCR-US96-06352-103 Sequence 103, App
31	32.8	2.8	2040	5	PCR-US96-06583-103 Sequence 10, Appl
32	32.4	2.8	1314	2	US-08-868-577-10 Sequence 10, Appl
33	32.4	2.8	1315	2	US-08-671-320-10 Sequence 18, Appl
34	32.4	2.8	3341	2	US-08-868-577-18 Sequence 1, Appl
35	32.2	2.8	1483	4	US-09-262-749-1 Sequence 1, Appl
36	32.2	2.8	1553	3	US-09-022-669-1 Sequence 1, Appl
37	32.2	2.8	1553	3	US-09-603-567-1 Sequence 5, Appl
38	31.8	2.7	44453	4	US-09-146-053-5 Sequence 245, App
39	31.6	2.7	521	4	US-08-991-789A-245 Sequence 245, App
40	31.6	2.7	521	4	US-09-062-451-245 Sequence 245, App
41	31.6	2.7	521	4	US-09-598-326-245 Sequence 1, Appl
42	31.6	2.7	2169	1	US-08-379-496-1 Sequence 1, Appl
43	31.4	2.7	248	4	US-09-007-005-32 Sequence 32, Appl
44	31.4	2.7	248	4	US-09-244-796-32 Sequence 3, Appl
45	31.4	2.7	277	4	US-09-007-005-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA: USN 60/064,671
APPLICATION NUMBER: 14 OCTOBER 1997
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA: USN 08/813,509
APPLICATION NUMBER: 07 MARCH 1997
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA: USN 08/772,330
APPLICATION NUMBER: 23 DECEMBER 1996
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

	Conservative	0;	Mismatches	65;	Indels	8;	Gaps
Qy	465	CAGAGAAAGTATTTTGGCTAAAGATGGCAATGCTTACCGCTAGAGCCTTCACATCTGTGTA	524				
Db	449	CATGGTTTGAATCTGGCCAGAGGAGCAGACGTTGTAACCTTAGGCTTTTGGCTATCTACATA	508				
Qy	525	TTTAATACCATCAATATCCCATGAGGCT--CATAAACAGAGTCTTCTCTTGGAACATG	582				
Db	509	TTATATCCACCCACATCCCATCTGGTTGCCATAAAGTAGTGTGCTCTGTGTAACATG	568				
Qy	583	ACCAAGATTGGGCAACGCTCCACATGACTTTTCAGCAAGGAAACTAGAGATCA---	639				
Db	569	ATCGGGGTTGGGCCAAGATCTCTCCACATGACTTTTAGCAATGAAACTATATGTTATATC	628				
Qy	640	---AAGGATTTTATTAACCGGAATCCGACATTTGGCTCTCGACATCGGGTATACCTCAGAC	696				
Db	629	AGGATGGCTTTTATTTACTTGATGTCCAACATTTGGCTTGCACATTCATGAAACTTCAGAG	688				
Qy	697	GCGTAACTCTGCAGACCTTCAGCTA	722				
Db	689	ACCTAGCTACAGATATCTTCAACTA	714				

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? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 954 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? IMMEDIATE SOURCE:
? LIBRARY:
? CLONE: huRANKL (full length)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..951
? IS-08-995-650.0

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LOCATION: 1..951
US-08-995-650-13

Query Match	10.98;	Score 126;	DB 4;	Length 954;
Best Local Similarity	72.68;	Pred. No. 1	46-31	
Matches 193.	Cons.			

		Indels	Gaps
QY	465 CAGGACAGATATTTGCTAAGAAATGGCAATCCGACGCTCAGCCTCAGCCTCAACTCATCTTGTTA	85	2
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Db	509 TTATATGCCACGACATCCCATCTGTTCCCATTAAGAGAGTGTCTCTTGTGTACCATG	582	
QY	583 ACCAAGATTGGCAAAAGCTCTCCAAAGTACTTCACGACAGGAAAACTAAGGTA---	568	
Db	569 ATCGGGGTTGGCCCAATATCTCCCAATGACTTTTATGCAATGGAAAAATATAAGTTATC	639	
QY	640 ---AAGCATTTATTTACCGGATGCGACACTTGTCTCTGACATGCGGTAACTCAGAG	628	
Db	629 AGGATGCGCTTTTATTTACCTGTATGCCAACATTTGCTTTGACATCATGAAACTTCAGAG	696	
QY	697 GCGTAACTCTGCAGGAGCTTCAGCTA 722	688	
Db	689 ACCTACCTACAGAGTATCTTCAACTA 714		

SUBJ: 3
09-215-649A-12
Sequence 12, Application US/09215649A
Patent No. 6271349
GENERAL INQUIRY

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SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-215-649A-12
Query Match 10.9%; Score 126; DB 4; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.4e-31;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;
QY 465 CAGGAGAAGTATTGCTAAGAAATGCAATGCTGAGCTGCTCAACTCATCTTGTTA 524
DB 449 CATGGTTAGATCTGGCCAGAGAGAGAGAGCTTGAAGCTCAGCTTTGGCATCTCAGTA 508
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAACGAGCTTTCTTCTTGGAAACATG 582
DB 509 TTATATGCACGACATCCCATCTGCTCCATTAAGTAGAGTCTGCTCTTGGTACCATG 568
QY 583 ACCAAGATTGGGCAACAGCTTCCCAACTGACTTTCAGCAACGAAAGAACTAAGTCA--- 639
DB 569 ATCGGGGTGGGCCAAGATCTCCCAACATGACTTTTACCAATGGAAGAACTAATGTTATC 628
QY 640 ---AAGGATTATTACCGGAATCCGCAATTTGCTCTCGACATCGGCTAACTCAGCAG 696
DB 629 AGGATGGCTTTATTAATCTGATGCAACATTTCTTTCGACATCAAGAACTCAGAG 688
QY 697 GCCTAACTCTGCAGACCTTCAGCTA 722
DB 689 ACCTAGCTACAGATATCTTCACTA 714
RESULT 4
US-09-577-780-12
Sequence 12, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galbert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-577-780-12
Query Match 10.9%; Score 126; DB 4; Length 954;
Best Local Similarity 72.6%; Pred. No. 1.4e-31;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;
QY 465 CAGGAGAAGTATTGCTAAGAAATGCAATGCTGAGCTGCTCAACTCATCTTGTTA 524
DB 449 CATGGTTAGATCTGGCCAGAGAGAGAGAGCTTGAAGCTCAGCTTTGGCATCTCAGTA 508
QY 525 TTATACCATCAATATCCCATGAGGCT--CATAAACGAGCTTTCTTCTTGGAAACATG 582
DB 509 TTATATGCACGACATCCCATCTGCTCCATTAAGTAGAGTCTGCTCTTGGTACCATG 568
QY 583 ACCAAGATTGGGCAACAGCTTCCCAACTGACTTTCAGCAACGAAAGAACTAAGTCA--- 639
DB 569 ATCGGGGTGGGCCAAGATCTCCCAACATGACTTTTACCAATGGAAGAACTAATGTTATC 628
QY 640 ---AAGGATTATTACCGGAATCCGCAATTTGCTCTCGACATCGGCTAACTCAGCAG 696
DB 629 AGGATGGCTTTATTAATCTGATGCAACATTTCTTTCGACATCAAGAACTCAGAG 688
QY 697 GCCTAACTCTGCAGACCTTCAGCTA 722
DB 689 ACCTAGCTACAGATATCTTCACTA 714

Db 689 ACCTAGCTACAGAGTATCTTCACTA 714

RESULT 5

US-09-052-521C-3
Sequence 3, Application US/09052521C
Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052, 521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880, 855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842, 842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 3
LENGTH: 2271
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (185)..(1135)
US-09-052-521C-3

Query Match 10.9%; Score 126; DB 4; Length 2271;
Best Local Similarity 72.6%; Pred. No. 2,4e-31;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAGAGTATTGCTTAAGATGGCAATCCGCTCAGCTCACTCACTCATCTGTGA 524
DB 633 CAGGTGATGATCTGGCCAGAGGAGCAAGCTGAAGCTCAGCTTTCCTCATCTCACTA 692
QY 525 TTATACCATCAATATCCATGAGGCT--CATAAAGCATCTTCTTCTGGAACATG 582
DB 693 TTATGCGACGACATCCATCTGTTCCATTAAGTGAAGTCTGCTCTTGGTACCAG 752
QY 583 ACCAAGTTGGCAACGCTGTCACATGACTTTCAGCAAGGAAACTAAGATCA--- 639
DB 753 ATCGGGGTGGGCCAAGATCTCCACATGACTTTAGCAATGGAATAATGTTAAATC 812
QY 640 ---AAGGCATTTTATCCGGAATCCGACATTTGCTGACATGCCGTAACCTGACAG 696
DB 813 AGATGGCTTTTATACCTGTATGCGAAGATTTGCTTGCACATCATGAACCTCAGAG 872
QY 697 GCCTAAGCTGCGAGACCTTCAGCTA 722
DB 873 ACCTAGCTACAGAGTATCTTCACTA 898

RESULT 6

US-08-996-139-10
Sequence 10, Application US/08996139
Patent No. 6017729

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Markovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Mus musculus

IMMEDIATE SOURCE:
LIBRARY:

CLONE: RANL
FEATURE:

NAME/KEY: CDS
LOCATION: 3..884

US-08-996-139-10

Query Match 8.4%; Score 97; DB 3; Length 1630;
Best Local Similarity 67.2%; Pred. No. 8e-22;
Matches 170; Conservative 0; Mismatches 75; Indels 8; Gaps 2;

QY 477 TTGCTAAGAAATGGCAATCTGACGCTCAGCCTCACTCATCTGTTAATACATCA 536
DB 394 TGGCCACAGGAGCAAGCCTGAGGCCCGCATTTGCACACCTCACCATCACTGCCA 453
QY 537 ATATCCCATGAGG--CTCATAAACGAGTCTTCTTCTTGGAAACATGACCAAGATTGG 594
DB 454 GCATCCCATGGGTTCCCATAAATGCTCTGCTCTTGGTACACAGATCGAGGCTGG 513
QY 595 CAAACGCTCCACATGACTTTCAGCAACGAAACTAAGATCA-----AAGCATTT 648
DB 514 CCAAGATCTCTAATCATGACGTTAGCAACGAAACTAAGGTTAACCAAGATGGCTTCT 573
QY 649 ATTACCGGAATGCCGACATTTGCTGACATGCGCTAAGCTTCAAGAGCCTTACTGTC 708
DB 574 ATTACCTGTACCCCAATATTGCTTTCGATCATGAACATCGGAGGAGCTACTACAG 633
QY 709 AGGACCTTCAGCT 721
DB 634 ACTATCTTCAGCT 646

RESULT 7

US-08-995-659-10
Sequence 10, Application US/08995659
Patent No. 6242213

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent

8.48; Score 97; DB 2; Length 2295;

Qy	477	TTCTTAAGATGGCAATCCTGACGCTACGCTTCAACGATCTTGTAATTAATACATCA	536
Db	615	TGGCCAGGAGGCAAGCCTGAGGCCACCATTTGGCACACTCACCATCAATCTGTCCA	674
Qy	537	ATATCCCATAGAG--CTCATAAACGAGTCCTTCTTCTTGAAACATGACCAGATTGGG	594
Db	675	GCATCCCATGGGTTCCCATTAAGTACACTCTGCTCTTGGTACCCAGATGAGGCTGGG	734
Qy	595	CAAAAGCTCCAAACATGACTTTCAGAACGGAACCTAAGAGTCA-----AAGCATTT	648
Db	735	CCAAGATCTCTAACTAGACGTTAAGCAACGGAAAACTAAGGTTTAACCAAATGGCTTCT	794
Qy	649	ATTACCGGAATGGCGACATTTGGCTCTCGACATCGCGTAACCTCAGACGCTAACTGTC	708
Db	795	ATTACGTGACGCCAACATTTGCTTCCGCAATCAAGAACAATCGGGAAGCGTACTCTACAG	854
Qy	709	AGGACCTTCAGCT 721	
Db	855	ACTATCTTCAGCT 867	

[illegible]

Query Match	3.2%;	Score 37;	DB 4;	Length 289;
Best Local Similarity	4.6%;	Pred. No. 0.021;		
Matches 10;	Conservative 98;	Mismatches 109;	Indels 0;	Gaps 0

RESULT 15
US-09-244-796-17
; Sequence 17, Application US/09244796
; Patent No. 6261344
; GENERAL INFORMATION:
; APPLICANT: Szoostak, Jack W.
; APPLICANT: Roberts, Richard W.

```

; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ. ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match      3.28; Score 37; DB 4; Length 289;
Best Local Similarity 4.6%; Pred. No. 0.021;
Matches 10; Conservative 98; Mismatches 109; Indels 0; Gaps 0;

QY 829 AGAGCTGAGAAGAGGGCCAGAGTGTCTGCTGACTGTGAGCCCGGAGAGCAGGAG 888
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DB 1  KGRGRARARARARURURARURURARURURARARARURURARARURGRNRN 60
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QY 889 TGGGTGCTGGGCTGAGAACCAAGTATGCGCCCTGGGAGCGCCGGGAGAGATGAGT 948
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 61 RSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRN 120
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
QY 949 TTTGAGCAAGGATTTGCAATTTGTGATGACTTGTGTGCTGAGAGGCTGAGAGT 1008
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 121 RSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRN 180
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
QY 1009 TGTACTCTGAGACAGACAGCAAGCATGATGATGATG 1045
   :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|: :|:|:
DB 181 RSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRSRNRRN 217
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 Job time : 91.8321 secs

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Tue Dec 10 10:51:37 2002

us-09-880-457-1_copy_543_746.nri

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:19 ; Search time 11.9188 Seconds
(without alignments)
5249.015 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204

Sequence: 1 catgagcctcataaagag.....gtatttgagatcattcac 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	96.4	47.3	954	3	US-08-996-139-12	Sequence 12, Appl
2	96.4	47.3	954	4	US-08-995-659-12	Sequence 12, Appl
3	96.4	47.3	954	4	US-09-215-649A-12	Sequence 12, Appl
4	96.4	47.3	954	4	US-09-577-780-12	Sequence 12, Appl
5	96.4	47.3	2271	4	US-09-052-521C-3	Sequence 3, Appl1
6	80.8	39.6	1630	3	US-08-996-139-10	Sequence 10, Appl
7	80.8	39.6	1630	4	US-08-995-659-10	Sequence 10, Appl
8	80.8	39.6	1630	4	US-09-215-649A-10	Sequence 10, Appl
9	80.8	39.6	2191	4	US-09-577-780-10	Sequence 10, Appl
10	80.8	39.6	2295	2	US-08-989-362-1	Sequence 6, Appl1
11	80.8	39.6	2295	2	US-08-842-842-6	Sequence 6, Appl1
12	80.8	39.6	1461	1	US-09-052-521C-1	Sequence 5, Appl1
13	80.8	39.6	1461	1	US-07-968-971A-5	Sequence 4, Appl1
14	29.4	14.4	1461	1	US-07-824-247-47	Sequence 7, Appl1
15	29.4	14.4	1461	1	US-08-142-473A-9	Sequence 9, Appl1
16	29.4	14.4	1461	1	US-08-464-523B-7	Sequence 9, Appl1
17	29.4	14.4	1461	1	US-08-469-203A-7	Sequence 7, Appl1
18	29.4	14.4	1461	1	US-08-470-204A-47	Sequence 7, Appl1
19	29.4	14.4	1461	3	US-08-926-522-12	Sequence 47, Appl
20	29.4	14.4	1461	3	US-08-768-964-14	Sequence 12, Appl
21	28.4	13.9	522	2	US-08-768-964-15	Sequence 14, Appl
22	28.4	13.9	522	2	US-08-768-964-15	Sequence 15, Appl
23	28.4	13.9	522	3	US-09-005-299-14	Sequence 14, Appl
24	28.4	13.9	522	3	US-09-005-299-15	Sequence 15, Appl
25	28.4	13.9	522	4	US-09-515-431-14	Sequence 14, Appl
26	28.4	13.9	522	4	US-09-515-431-15	Sequence 15, Appl
27	28.4	13.9	597	2	US-08-768-964-11	Sequence 11, Appl

C 28	28.4	13.9	597	2	US-08-768-964-16	Sequence 16, Appl
C 29	28.4	13.9	597	3	US-09-005-299-11	Sequence 11, Appl
C 30	28.4	13.9	597	3	US-09-005-299-16	Sequence 16, Appl
C 31	28.4	13.9	597	4	US-09-515-431-11	Sequence 11, Appl
C 32	28.4	13.9	597	4	US-09-515-431-16	Sequence 16, Appl
C 33	28.4	13.9	714	2	US-08-768-964-8	Sequence 8, Appl1
C 34	28.4	13.9	714	3	US-09-005-299-6	Sequence 6, Appl1
C 35	28.4	13.9	714	3	US-09-005-299-8	Sequence 8, Appl1
C 36	28.4	13.9	714	4	US-09-515-431-6	Sequence 6, Appl1
C 37	28.4	13.9	714	4	US-09-515-431-8	Sequence 8, Appl1
C 38	28.4	13.9	789	2	US-08-768-964-4	Sequence 4, Appl1
C 39	28.4	13.9	789	2	US-08-768-964-5	Sequence 5, Appl1
C 40	28.4	13.9	789	3	US-09-005-299-4	Sequence 4, Appl1
C 41	28.4	13.9	789	3	US-09-005-299-5	Sequence 5, Appl1
C 42	28.4	13.9	789	4	US-09-515-431-5	Sequence 5, Appl1
C 43	28.4	13.9	789	4	US-09-515-431-5	Sequence 5, Appl1
C 44	28.4	13.9	789	4	US-09-515-431-5	Sequence 5, Appl1
C 45	28.4	13.9	1069	2	US-08-768-964-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Markovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-996-139-12

Query Match 47.3% Score 96.4; DB 3; Length 954;
Best Local Similarity 74.5%; Pred. No. 3.7e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATATAAAGAGAGCTTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTC 62
DB 531 TGGTCCCAATAAGTAGCTGCTCTCTGTCATGATGAGGCTGGGCAAGATCTC 116
QY 63 CAACATGACTTTGAGCAAGGAAAGTAAAGTCA-----AAGCATTTATTACCGGAA 116
DB 591 CAACATGACTTTGAGCAAGGAAAGTAAAGTCA-----AAGCATTTATTACCGGAA 116
QY 117 TGCCGACATTTGCTTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTTACCTGTA 650
DB 651 TGCCGACATTTGCTTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTTACCTGTA 650
QY 177 GCTA 180
DB 711 ACTA 714

RESULT 2

US-08-995-659-12
Sequence 12, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY:
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
US-08-995-659-12

Query Match 47.3% Score 96.4; DB 4; Length 954;
Best Local Similarity 74.5%; Pred. No. 3.7e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATATAAAGAGAGCTTTCTTCTTGAAACATGACCAAGATTGGGCAACGCTTC 62
DB 531 TGGTCCCAATAAGTAGCTGCTCTCTGTCATGATGAGGCTGGGCAAGATCTC 116
QY 63 CAACATGACTTTGAGCAAGGAAAGTAAAGTCA-----AAGCATTTATTACCGGAA 116
DB 591 CAACATGACTTTGAGCAAGGAAAGTAAAGTCA-----AAGCATTTATTACCGGAA 116
QY 117 TGCCGACATTTGCTTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTTACCTGTA 650
DB 651 TGCCGACATTTGCTTCGACATGCGCTAAGCTCAGAGGCTTAAGTCTTACCTGTA 650
QY 177 GCTA 180
DB 711 ACTA 714

RESULT 3

US-09-215-649A-12
Sequence 12, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>

Tue Dec 10 10:51:37 2002

us-09-880-457-1-copy_543_746.rni

Page 3

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-215-649A-12

Query Match 47.3%; Score 96.4; DB 4; Length 954;
Best Local Similarity 74.5%; Pred. No. 3.7e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
QY 3 TGAGGCTCATAAAGAGTCTTCTTCTTGGAAACATGACCAAGATGGGCAACGCTTC 62
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DB 531 TGTTCCATTAAGAGTCTGCTCTTGTGACCATGATCGGGTTGGCCCAAGATCTC 590
QY 63 CAACATGACTTTCAGCAACGGAAGTAAGATCA-----AAGCATTTATTACCGGAA 116
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 591 CAACATGACTTTCAGCAACGGAAGTAAGATCA-----AAGCATTTATTACCGGAA 116
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QY 117 TGCCGACATTTGCTCGACATCGGTAACCTCAGCAGGCTTAACCTCGAGGACCTTCA 176
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 651 TGCCGACATTTGCTCGACATCATGAACCTCAGGAGACCTAGCTACAGAGTATCTTCA 710
QY 177 GCTA 180
|||
DB 711 ACTA 714

RESULT 4
US-09-577-780-12
Sequence 12, Application US/09577780
Patent No. 6419928
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-577-780-12

Query Match 47.3%; Score 96.4; DB 4; Length 954;
Best Local Similarity 74.5%; Pred. No. 3.7e-26;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
QY 3 TGAGGCTCATAAAGAGTCTTCTTCTTGGAAACATGACCAAGATGGGCAACGCTTC 62
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 531 TGTTCCATTAAGAGTCTGCTCTTGTGACCATGATCGGGTTGGCCCAAGATCTC 590
QY 63 CAACATGACTTTCAGCAACGGAAGTAAGATCA-----AAGCATTTATTACCGGAA 116
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 591 CAACATGACTTTCAGCAACGGAAGTAAGATCA-----AAGCATTTATTACCGGAA 116
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QY 117 TGCCGACATTTGCTCGACATCGGTAACCTCAGCAGGCTTAACCTCGAGGACCTTCA 176
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DB 651 TGCCGACATTTGCTCGACATCATGAACCTCAGGAGACCTAGCTACAGAGTATCTTCA 710
QY 177 GCTA 180
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DB 711 ACTA 714

RESULT 5
US-09-052-521C-3
Sequence 3, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451BIV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842

;; PRIOR FILING DATE: 1997-04-16
;; NUMBER OF SEQ ID NOS: 40
;; SOFTWARE: Patentl Ver. 2.1
;; SEQ ID NO 3
;; LENGTH: 2271
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (185)..(1135)
US-09-052-521C-3

Query Match
Best Local Similarity 47.3%; Score 96.4; DB 4; Length 2271;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATATAACGAGCTTCTCTCTGGAACATGACCAAGATTGGGCAACGCTC 62
DB 715 TGGTCCCATTAAGTAGTGTCTCTGTCATGATCGGGTGGGCCAAGATCTC 774
QY 63 CAACATGACTTTCAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGAA 116
DB 775 CAACATGACTTTCAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGAA 116
QY 117 TGGCAGATTGCTCTGACATCGGTAACCTCAGCAGCCTTAAGCTGACGAGCTTCA 834
DB 835 TGGCAGATTGCTCTGACATCGGTAACCTCAGCAGCCTTAAGCTGACGAGCTTCA 176
QY 177 GCTA 180
DB 895 ACTA 898

RESULT 6
US-08-996-139-10

;; Sequence 10, Application US/08996139
;; Patent No. 6017729
;; GENERAL INFORMATION:

;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/996,139
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1630 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Mus musculus
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE: RANKL
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..884
US-08-996-139-10

Query Match
Best Local Similarity 39.6%; Score 80.8; DB 3; Length 1630;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 8 CTCATTAACGAGCTTCTCTCTTGGAAACATGACCAAGATTGGGCAACGCTCCACA 67
DB 469 CCCATTAAGTCACTCTGCTCTTGTACACGATGAGGCTGGCCCAAGATCTTACA 528
QY 68 TGACTTTCAGCAGGAAACTAAGTCA-----AAGCATTTATTTACCGGAATGCCG 121
DB 529 TGACGTTAAGCAGGAAACTAAGGTTAACCAAGATGGCTTCTATTAAGCTTACGCA 588
QY 122 ACATTGCTCTGACATCGGTAACCTCAGCAGCCTTAAGCTGACGAGCTTCA 179
DB 589 ACATTGCTCTGACATCGGTAACCTCAGCAGCCTTAAGCTGACGAGCTTCA 646

RESULT 7
US-08-995-659-10

;; Sequence 10, Application US/08995659
;; Patent No. 6242213
;; GENERAL INFORMATION:

;; APPLICANT: Anderson, Dirk M.
;; APPLICANT: Galibert, Laurent
;; APPLICANT: Maraskovsky, Eugene
;; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/995,659
;; FILING DATE: 22 DECEMBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:

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1      APPLICATION NUMBER: 08/996,139
2      FILING DATE: <Unknown>
3      APPLICATION NUMBER: USN 08/813,509
4      FILING DATE: 07 MARCH 1997
5      APPLICATION NUMBER: USN 08/772,330
6      FILING DATE: 23 DECEMBER 1996
7      ATTORNEY/AGENT INFORMATION:
8      NAME: Perkins, Patricia Anne
9      REGISTRATION NUMBER: 34,693
10     REFERENCE/DOCKET NUMBER: 2851-A
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE: (206)587-0430
13     TELEFAX: (206)233-0644
14     INFORMATION FOR SEQ ID NO: 10:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 1630 base pairs
17     TYPE: nucleic acid
18     STRANDEDNESS: single
19     TOPOLOGY: linear
20     MOLECULE TYPE: cDNA
21     HYPOTHETICAL: NO
22     ANTI-SENSE: NO
23     ORIGINAL SOURCE:
24     ORGANISM: Mus musculus
25     IMMEDIATE SOURCE:
26     LIBRARY: <Unknown>
27     CLONE: RANKL
28     FEATURE:
29     NAME/KEY: CDS
30     LOCATION: 3..884
31     SEQUENCE DESCRIPTION: SEQ ID NO: 10:
32     US-09-215-669A-10
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Query Match	Similarity	39.6%;	Score 80.8;	DB 4;	Length 1050;
Best Local	Similarity	70.2%;	Pred. No. 3.2e-20;		
Matches	Conservative	0;	Mismatches 47;	Indels	Gaps
QY	8	CTCATAAACGAGTCTTCTTCTTGGAACATACCAAGATTGGGCAACGCTCTCCACA	67		
Db	469	CCCATTAATCATCTGTCTCTCTTGTCACGATCGAGGCTGGGCGCAAGTCTCTACAA	528		
QY	68	TGACTTTCGCAAGGAAACTAGATATCA-----AAGCATTTATTACGGAAATCGCG	121		
Db	529	TGACGTTAAGCAACGAAACTAAGGGTTAACCAAGTGGCTTCTATTACGTGACGCA	588		
QY	122	ACATTTCCTCTCGACATGCGCTTAACCTCAGACGAGGCTTAATCTGCAGGACCTTCAGCT	179		
Db	589	ACATTTCCTTCGGGATCATGAAACATCGGGGAACGCTACTACAGACATCTTCACGCT	646		

? RESULT 9
 ? US-09-577-780-10
 ? Sequence 10, Application US/09577780
 ? Patent No. 6419929
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: Anderson, Dirk M.
 ? Galibert, Laurent
 ? Marashevsky, Eugene
 ?
 ? TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
 ?
 ? NUMBER OF SEQUENCES: 19
 ?
 ? CORRESPONDENCE ADDRESSES:
 ? ADDRESSEE: Immunex Corporation, Law Department
 ? STREET: 51 University Street
 ? CITY: Seattle
 ?
 ? STATE: WA
 ?
 ? COUNTRY: USA
 ?
 ? ZIP: 98101
 ?
 ? COMPUTER READABLE FORM:
 ?
 ? MEDIUM TYPE: Floppy disk
 ?
 ? COMPUTER: Apple Power Macintosh
 ?
 ? OPERATING SYSTEM: Apple Operating System 7.5.5
 ?
 ? SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 ?
 ? CURRENT APPLICATION DATA:
 ?
 ?

APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-577-780-10

Query Match
Best Local Similarity 39.6%; Score 80.8; DB 4; Length 1630;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

DB 8 CTCATAAAGAGCTCTTCTTGTGAAACATGACCAAGATTGGGCAACGCTCCACA 67
469 CCCATAAGTCACTCTCTCTTGTGACGATGAGGCTGGGCCAAGATCTTAACA 528
QY 68 TGACTTTCACACGGAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAATGCCG 121
DB 529 TGACGTTAAGCAACGGAAGAACTAAGGTTAACCAAGATGGCTTCTATTACTGTACGCCA 588
QY 122 ACATTGCTCTGCACATCGGTAACCTCAAGAGGCTTAACCTTGACGAGCTTACGCT 179
DB 589 ACATTGCTTTCGATCATGAACATCGGGAAGGCTTACCTACAGACTATCTTACGCT 646

RESULT 10
US-08-989-362-1
Sequence 1, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Matison, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)496-1204
TELEFAX: (650)852-9196
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 125..1072
US-08-989-362-1

Query Match
Best Local Similarity 39.6%; Score 80.8; DB 4; Length 2191;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

DB 8 CTCATAAAGAGCTCTTCTTGTGAAACATGACCAAGATTGGGCAACGCTCCACA 67
DB 657 CCCATAAGTCACTCTCTCTTGTGACGATGAGGCTGGGCCAAGATCTTAACA 716
QY 68 TGACTTTCACACGGAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAATGCCG 121
DB 717 TGACGTTAAGCAACGGAAGAACTAAGGTTAACCAAGATGGCTTCTATTACTGTACGCCA 776
QY 122 ACATTGCTCTGCACATCGGTAACCTCAAGAGGCTTAACCTTGACGAGCTTACGCT 179
DB 777 ACATTGCTTTCGATCATGAACATCGGGAAGGCTTACCTACAGACTATCTTACGCT 834

RESULT 11
US-08-842-842-6
Sequence 6, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451

Patent No. 5512482
GENERAL INFORMATION:
APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/824,247
FILING DATE: 19920122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
FILING DATE: 24-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
FILING DATE: 7-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/704,861
FILING DATE: 21-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02960
FILING DATE: 25-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,007
FILING DATE: 27-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,426
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/514,030
FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 82-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: PCR product from mRNA template
US-07-824-247-47

Query Match 14.4%; Score 29.4; DB 1; Length 1461;
Best Local Similarity 56.8%; Pred. No. 0.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 10 CATAAAGAGCTCTTCTCTGGAACATGACCAAGATTGGGCAACGCTCCACATG 69
DB 1241 CAGAAATCAGGCTGTGGTTTATGATATATATCCAAATTTGCTATATCTCAAGAACTT 1300
QY 70 ACTTTAGCAACGGAAGAACTAAGAGTCAAGGCAT 104
DB 1301 AATATCAGAAATAATACATGAGTCAAGTTAT 1335

RESULT 15
US-08-142-473A-7
Sequence 7, Application US/08142473A
Patent No. 5639790
GENERAL INFORMATION:
APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
COMPUTER: Apple Macintosh IICx
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,473A
FILING DATE: 18-NOV-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04332
FILING DATE: 21-MAY-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/824,247
FILING DATE: 22-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
FILING DATE: 24-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
FILING DATE: 7-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/704,861
FILING DATE: 21-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 82-4 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-08-142-473A-7

Query Match 14.4%; Score 29.4; DB 1; Length 1461;
Best Local Similarity 56.8%; Pred. No. 0.4;
Matches 54; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 10 CATAAAGAGCTCTTCTCTGGAACATGACCAAGATTGGGCAACGCTCCACATG 69
DB 1241 CAGAAATCAGGCTGTGGTTTATGATATATATCCAAATTTGCTATATCTCAAGAACTT 1300
QY 70 ACTTTAGCAACGGAAGAACTAAGAGTCAAGGCAT 104
DB 1301 AATATCAGAAATAATACATGAGTCAAGTTAT 1335

Tue Dec 10 10:51:37 2002

Search completed: December 8, 2002, 17:28:32
Job time : 17.918 secs

us-09-880-457-1_copy_543_746.rni

111

Tue Dec 10 10:51:46 2002

US-09-880-457-4_COPY_20_87.rapb

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 8, 2002, 19:31:38 ; Search time 10.0903 Seconds
(without alignments)
109,459 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAKTSLSSWKHDQMANV.....TSAGTLTDLQDLMCNRIH 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PublishedApplications_AA.*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCOT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
11: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	373	100.0	87	10 US-09-880-457-4	Sequence 4, App1
2	358	96.0	94	10 US-09-880-457-5	Sequence 5, App1
3	358	96.0	95	10 US-09-880-457-6	Sequence 6, App1
4	178	47.7	160	9 US-09-779-050A-15	Sequence 15, App1
5	178	47.7	317	9 US-09-877-650-13	Sequence 13, App1
6	178	47.7	317	10 US-09-871-856-13	Sequence 13, App1
7	178	47.7	317	10 US-09-871-856-13	Sequence 2, App1
8	174	46.6	245	9 US-10-017-910-2	Sequence 14, App1
9	172	46.1	160	9 US-09-779-050A-14	Sequence 11, App1
10	172	46.1	294	9 US-09-871-856-11	Sequence 11, App1
11	172	46.1	316	9 US-10-017-910-4	Sequence 8, App1
12	112.5	30.2	109	10 US-09-911-777-8	Sequence 5085, Ap
13	112.5	30.2	813	10 US-09-815-242-5085	Sequence 5, App1
14	63.5	17.0	329	10 US-09-924-841-9	Sequence 9, App1
15	59.5	16.0	329	10 US-09-924-841-9	Sequence 334, App
16	59.5	15.0	484	10 US-09-801-368-334	Sequence 1, App1
17	56	14.9	679	12 US-10-119-714-1	Sequence 760, App
18	55.5	14.9	753	10 US-09-925-302-760	
19	55.5	14.9	753	10 US-09-925-302-760	

20	55	14.7	57	10 US-09-864-761-42649	Sequence 42649, A
21	54.5	14.6	333	10 US-09-924-841-10	Sequence 10, App1
22	54	14.5	146	9 US-09-779-050A-10	Sequence 16, App1
23	54	14.5	149	10 US-09-934-465-16	Sequence 2, App1
24	54	14.5	261	10 US-09-842-745A-2	Sequence 10, App1
25	54	14.5	323	10 US-09-280-197-10	Sequence 2, App1
26	54	14.5	1091	9 US-09-423-126-2	Sequence 39850, A
27	54	14.5	1091	10 US-09-280-197-2	Sequence 4, App1
28	53	14.2	77	10 US-09-864-761-39850	Sequence 4, App1
29	53	14.2	204	10 US-09-866-582-4	Sequence 4, App1
30	53	14.2	220	9 US-10-133-178-4	Sequence 4, App1
31	53	14.2	764	10 US-09-747-521-4	Sequence 4, App1
32	53	14.2	764	10 US-10-106-014-4	Sequence 4, App1
33	53	14.2	1136	10 US-09-815-242-12447	Sequence 12447, A
34	53	14.2	1136	10 US-09-815-242-12814	Sequence 12814, A
35	53	14.2	1179	9 US-09-815-242-5522	Sequence 5522, Ap
36	52.5	14.1	577	9 US-10-047-542-66	Sequence 66, App1
37	52	13.9	261	10 US-09-245-764-7	Sequence 7, App1
38	52	13.9	294	10 US-10-027-806-12	Sequence 12, App1
39	52	13.9	593	10 US-09-943-446-9	Sequence 9, App1
40	52	13.9	595	10 US-09-943-446-6	Sequence 36, App1
41	52	13.9	953	10 US-09-354-453-36	Sequence 16, App1
42	51.5	13.8	972	10 US-09-924-154-16	Sequence 2, App1
43	51	13.7	318	12 US-10-032-626-2	Sequence 422, App
44	51	13.7	394	9 US-09-992-598-422	Sequence 422, App
45	51	13.7	394	9 US-09-989-293A-422	

ALIGNMENTS

RESULT 1
US-09-880-457-4 Application US/09880457
Sequence 4, App1
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 4
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-4

Query Match 100.0%; Score 373; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 7.3e-41;
Matches 68; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HEAKTSLSSWKHDQMANVSMFESNGKLRKGYRNRADICSRHRYTSAGTLTDLQ 60
DB 20 HEAKTSLSSWKHDQMANVSMFESNGKLRKGYRNRADICSRHRYTSAGTLTDLQ 79

QY 61 WCNLRRIH 68
DB 80 WCNLRRIH 87

RESULT 2
US-09-880-457-5
Sequence 5, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey

```
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-5
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Query Match
Best Local Similarity 96.0%; Score 358; DB 10; Length 94;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 20 HEAHTSLSSMKHDDMANVSNMTFSGNKLRYKGIYRNADICSRHRYTSAGLTLDL 60
OY 61 WCNLRIT 67
DB 80 WCNLRSV 86
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RESULT 3
US-09-880-457-6
Sequence 6, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 6
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-6
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Query Match
Best Local Similarity 96.0%; Score 358; DB 10; Length 95;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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OY 1 HEAHTSLSSMKHDDMANVSNMTFSGNKLRYKGIYRNADICSRHRYTSAGLTLDL 60
DB 20 HEAHTSLSSMKHDDMANVSNMTFSGNKLRYKGIYRNADICSRHRYTSAGLTLDL 60
OY 61 WCNLRIT 67
DB 80 WCNLRSV 86
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RESULT 4
US-09-779-050A-15
Sequence 15, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAITING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
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CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-050A-15
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Query Match
Best Local Similarity 47.7%; Score 178; DB 9; Length 160;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
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OY 3 AHKTSLSMKHDDMANVSNMTFSGNKLRYKGIYRNADICSRHRYTSAGLTLDL 60
DB 22 SHKVSLSWYHDGMAKISNMTFSGNKLRYKGIYRNADICSRHRYTSAGLTLDL 81
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RESULT 5
US-09-877-650-13
Sequence 13, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maaskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0450
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13
```

```
Query Match
Best Local Similarity 47.7%; Score 178; DB 9; Length 317;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
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APPLICANT: MACKAY, Fabienne ;

ORGANISM: Pseu
US-09-815-242-5085

Query Match	17.0%;	Score 63.5;	DB 10;	Length 813;
Best Local Similarity	28.8%;	Pred. No. 3.5;		
Matches	19;	Conservative	11;	Mismatches 23;
				Indels 13;
				Gaps 3

RESULT 15
US-09-924-841-5
; Sequence 5, Application US/09924841
; Patent No. US20020127633A1
GENERAL INFORMATION

```

GENERAL INFORMATION:
APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
FILE REFERENCE: MS041-453
CURRENT APPLICATION NUMBER: US/09/924,841
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/413,231
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 329
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
NAME/KEY: M0TAGEN
LOCATION: (210)
OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-5

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Query Match          16.0%: Score 59.5; DB 10; Length 329;
Best Local Similarity 25.7%: Pred No. 3.7;
Matches 18; Conservative 10; Mismatches 33; Indels 9; Gaps 2

QY      1  HEAHTSLSSKWH-----QDMANVSMTFS--NGKLIRVGIYYRNADICSRRHRTSA  51
Db      60  NEFHGAMTDQEHNDLAIHYNPNDFHVRNGYKAVGRRKAVSFECYLNDDEGDHPMIA  119
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      52  GLTLDDLDLQ  61
Db     120  GTPHHEVNLW  129

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Search completed: December 8, 2002, 19:36:16
Job time : 11.0903 secs

RESULT 2
US-09-880-457-6
; Sequence 6, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey

APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 6
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-6

Query Match
Best Local Similarity 96.7%; Score 440; DB 10; Length 95;
Matches 84; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALTTLSLQILLIPISHEAKHTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
DB 1 MALTTLSLQILLIPISHEAKHTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
QY 61 ICSRHRVTSAGLTLDLQDLMCNLRV 86
DB 61 ICSRHRVTSAGLTLDLQDLMCNLRV 86

RESULT 3
US-09-880-457-5
Sequence 5, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-457-5

Query Match
Best Local Similarity 95.4%; Score 434; DB 10; Length 94;
Matches 83; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALTTLSLQILLIPISHEAKHTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
DB 1 MALTTLSLQILLIPISHEAKHTSLSSWKHDQDANVSNMTFSGKLRVAGIYRNAD 60
QY 61 ICSRHRVTSAGLTLDLQDLMCNLRV 86
DB 61 ICSRHRVTSAGLTLDLQDLMCNLRV 86

RESULT 4
US-09-779-050A-15
Sequence 15, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A

CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-050A-15

Query Match
Best Local Similarity 39.7%; Score 180.5; DB 9; Length 160;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKHTSLSSWKHDQDANVSNMTFSGKLRV--GIYRNADICSHRVTSAGL 72
DB 18 IPSGS---HKVSLSSWYHDGRGAKISNMTFSGKLRVADGFRYLYANICFRHETSGL 74
QY 73 TLDDQL 79
DB 75 ATBYQL 81

RESULT 5
US-09-877-650-13
Sequence 13, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid

MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

Query Match 39.7%; Score 180.5; DB 9; Length 317;
Best Local Similarity 59.7%; Pred. No. 7e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAHTSLSMKHDDMANVSNMTPSNGKLRVK--GIYYRNADICSRHRTSAGL 72
||| | ||||| ||: ||||| ||| | ||| ||| ||| |
DB 175 IPSGS---HKVSLSSWYHDKGMAKISMNTPSNGKLIYNODGFYLLVNICFRHHETSGLD 231

QY 73 TLQDLQ 79
: |||
DB 232 ATEYLQ 238

RESULT 6
US-09-813-329-7
; Sequence 7, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
; FILE REFERENCE: D0016.0P
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match 39.7%; Score 180.5; DB 10; Length 317;
Best Local Similarity 59.7%; Pred. No. 7e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAHTSLSMKHDDMANVSNMTPSNGKLRVK--GIYYRNADICSRHRTSAGL 72
||| | ||||| ||: ||||| ||| | ||| ||| ||| |
DB 175 IPSGS---HKVSLSSWYHDKGMAKISMNTPSNGKLIYNODGFYLLVNICFRHHETSGLD 231

QY 73 TLQDLQ 79
: |||
DB 232 ATEYLQ 238

RESULT 7
US-09-871-856-13
; Sequence 13, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match 39.7%; Score 180.5; DB 10; Length 317;
Best Local Similarity 59.7%; Pred. No. 7e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAHTSLSMKHDDMANVSNMTPSNGKLRVK--GIYYRNADICSRHRTSAGL 72
||| | ||||| ||: ||||| ||| | ||| ||| ||| |
DB 175 IPSGS---HKVSLSSWYHDKGMAKISMNTPSNGKLIYNODGFYLLVNICFRHHETSGLD 231

QY 73 TLQDLQ 79
: |||
DB 232 ATEYLQ 238

RESULT 8
US-10-017-910-2
; Sequence 2, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:


```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-017-910-4

Query Match      38.7%;      Score 176;      DB 9;      Length 316;
Best Local Similarity 55.4%;      Pred. No. 2.5e-14;
Matches 36;      Conservative 6;      Mismatches 21;      Indels 2;      Gaps 1

QY      17      SISHAHKTSLSMKHODWANYSNMTFENGKLYRK--GIYYRNADICSRHRYTSAGILT 74
      ||:||||| ||: || :||||| ||||| || || ||: || || :
DB      173      SIPSQSHVYVTSWYHDHGRAKTSNMFTLSNGKLRVYVDGFYLYANICFRHHTSGSVPT 232

QY      75      QDLQL 79
      |||
DB      233      DYQL 237

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RESULT 13
US-09-911-777-8
; Sequence 8, Application US/09911777
; Patent No. US20020037852A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: APOTEC S. A.
APPLICANT: BROMNING, Jeffrey
APPLICANT: AMBROSE, Christine
APPLICANT: MACRAY, Fadienne
APPLICANT: TSCHOEP, Jurq
APPLICANT: SCHNEIDER, Pascal
TITLE OF INVENTION: BAF, Inhibitors Thereof and Their Use
TITLE OF INVENTION: In the Modulation of B-Cell Response
FILE REFERENCE: A070 US
CURRENT APPLICATION NUMBER: US/09/911,777
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/117,169
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 60/143,228
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: PCT/US00/01788
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo Sapien
US-09-911-777-8

      25.3%; Score 115; DB 10; Length 109;
Best Local Similarity 43.1%; Pred. No. 2,4e-07;
Matches 28; Conservative 4; Mismatches 15; Indels 18; Gaps 2

QY      15  TSIISHEAHKTSLSMKHDODAWANSNMTFENGKLRVKGIIYRNADICSRHRYTSAGLTL 74
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      15  IPBGS---HKVSLSMYHIDRGKGRKSNM-----YANICFRHHEHSGDLAT 56
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      75  ODQL 79
      : |||
DB      57  EYQL 61

RESULT 14
US-09-815-242-5085
; Sequence 5085, Application US/09815242

```

```
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Hasebeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA-011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5085
LENGTH: 813
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5085

Query Match
Best Local Similarity 14.0%; Score 63.5; DB 10; Length 813;
Matches 19; Conservative 11; Mismatches 23; Indels 13; Gaps 3;

QY 25 TSLSMKHDOPWANSNMTFSNGK-LRVKGT-----YYRNADICSRHRT---SAG 71
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 711 TAYLQYKPDADNNRLQATFDSKDYRLDGVSEFGRRQVSTYTVDLVSQYRITPDQLS 770
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 72 LTLDL 77
   | : | | |
Db 771 LGIONL 776

RESULT 15
US-09-924-841-5
Sequence 5, Application US/09924841
Patent No. US20020127633A1
GENERAL INFORMATION:
APPLICANT: Dilley, David R.
APPLICANT: Kadyrzhanova, Dina K
APPLICANT: Wang, Zhenyong
APPLICANT: Warner, Toni M
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and
FILE REFERENCE: MSU41-453
CURRENT APPLICATION NUMBER: US/09/924,841
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/413,231
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 329
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
NAME/KEY: MUTAGEN
LOCATION: (210)
OTHER INFORMATION: Glu210 in native IPNS modified to Arg
US-09-924-841-5

Query Match
Best Local Similarity 13.5%; Score 61.5; DB 10; Length 329;
Matches 18; Conservative 12; Mismatches 36; Indels 9; Gaps 2;

QY 15 IPSISHEAHTSLSWKHD-----QDMANYSNMTFS--NGRLRYKGIYYRNADICSRH 65
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 55 LDYVNEFHGAMTDQEKHDLAHAYPNDPNHHVNGYKAVPGKAVESFCYLNPDGEGDH 114
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 66 RYTSAGLTLQDLQDLW 80
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 PMIAAGTPMHVEVNLW 129
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Search completed: December 8, 2002, 19:36:15
Job time : 13.9097 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:18:27 ; Search time 11.9188 Seconds
(without alignments)
6674.007 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204
1 catgagcctcataaagcag.....gttaattgagatcatcacc 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications -NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	1161	10	US-09-880-457-1
2	194	95.1	1186	10	US-09-880-457-3
3	194	95.1	2412	10	US-09-880-457-2
4	96.4	47.3	954	9	US-09-877-650-12
5	96.4	47.3	954	10	US-09-871-856-12
6	93.2	45.7	1823	9	US-10-017-910-1
7	80.8	39.6	1630	9	US-09-877-650-10
8	80.8	39.6	1630	10	US-09-871-856-10
9	80.8	39.6	2237	9	US-10-017-910-3
10	61	29.9	493	10	US-09-880-457-9
11	31.2	15.3	985	9	US-10-040-739-93
12	31.2	15.3	985	10	US-09-920-300A-1691
13	31.2	15.3	985	12	US-10-033-528-1691
14	31.2	15.3	3073	10	US-09-867-701-10910
15	31.2	15.3	3073	10	US-09-920-300A-1690
16	31.2	15.3	3073	12	US-10-033-528-1690
17	30	14.7	30	10	US-09-880-457-8
18	29.4	14.4	409	10	US-09-783-590-1953
19	29.4	14.4	454	10	US-09-864-761-14164

C	20	29.4	14.4	2244	10	US-09-764-864-153	Sequence 133, App
	21	28.6	14.0	1365	10	US-09-815-242-4243	Sequence 4243, Ap
	22	28.6	14.0	1365	10	US-09-815-242-8196	Sequence 8196, Ap
	23	28.2	13.8	477	10	US-09-759-143-92	Sequence 92, Appl
	24	28.2	13.8	477	10	US-09-780-669-92	Sequence 92, Appl
	25	28.2	13.8	477	10	US-09-030-606-92	Sequence 92, Appl
	26	28.2	13.8	477	10	US-09-822-827-92	Sequence 92, Appl
	27	28.2	13.8	477	10	US-09-115-453-92	Sequence 92, Appl
	28	28.2	13.8	2000	9	US-09-938-842A-4251	Sequence 4251, Ap
	29	27.8	13.6	666	10	US-09-764-864-590	Sequence 590, Ap
	30	27.8	13.6	2048	10	US-09-764-847-1468	Sequence 1468, Ap
	31	27.8	13.6	465237	10	US-09-933-267A-1	Sequence 1, Appl
	32	27.6	13.5	371	10	US-09-834-975-285	Sequence 285, App
	33	27.6	13.5	608	10	US-09-759-143-193	Sequence 193, App
	34	27.6	13.5	608	10	US-09-780-669-193	Sequence 193, App
	35	27.6	13.5	608	10	US-09-030-606-193	Sequence 193, App
	36	27.6	13.5	608	10	US-09-822-827-193	Sequence 193, App
	37	27.6	13.5	608	10	US-09-115-453-193	Sequence 193, App
	38	27.6	13.5	909	10	US-09-935-943-7	Sequence 7, Appl
	39	27.6	13.5	1873	10	US-09-834-975-756	Sequence 756, App
	40	27.6	13.5	1873	10	US-09-834-975-757	Sequence 757, App
	41	27.2	13.3	817	10	US-09-809-545A-7	Sequence 7, Appl
	42	27.2	13.3	2000	9	US-09-938-842A-4387	Sequence 4387, Ap
	43	27	13.2	27	10	US-09-880-457-7	Sequence 7, Appl
	44	27	13.2	280	10	US-09-294-093B-5098	Sequence 5098, Ap
	45	27	13.2	9542	10	US-09-764-847-1809	Sequence 1809, Ap

ALIGNMENTS

RESULT 1
US-09-880-457-1
; Sequence 1, Application US/09880457
; Patient No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; TITLE OF INVENTION: For the Treatment of Body Weight Disorders
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-1

Query Match 100.0%; Score 204; DB 10; Length 1161;
Best Local Similarity 100.0%; Pred. No. 1.5e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CATGAGCCTCATAAACGAGCTCTTCTTGGAAACATGACCAATGGGCAACGTC	60
DB	543	CATGAGCCTCATAAACGAGCTCTTCTTGGAAACATGACCAATGGGCAACGTC	602
QY	61	TCACAACATGACTTTACGACCAAGAAACCTAAGAGGCAATTATACCGGATGCC	120
DB	603	TCACAACATGACTTTACGACCAAGAAACCTAAGAGGCAATTATACCGGATGCC	662
QY	121	GACATTTGCTCTGACACWCGCTAACCTCAGCAGGCTTAATCTGACGACCTTCAGCTA	180
DB	663	GACATTTGCTCTGACACWCGCTAACCTCAGCAGGCTTAATCTGACGACCTTCAGCTA	722
QY	181	TGGTGTATTTGAGATCATTCATC	204
DB	723	TGGTGTATTTGAGATCATTCATC	746

```

RESULT 2
US-09-880-457-3
: Sequence 3, Application US/09880457
: Patent No. US20020106728A1
: GENERAL INFORMATION:
: APPLICANT: Pan, James
: APPLICANT: Goddard, Audrey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
: FILE REFERENCE: P287191
: CURRENT APPLICATION NUMBER: US/09/880,457
: PRIOR FILING DATE: 2001-06-12
: PRIOR APPLICATION NUMBER: US 60/212,901
: NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 3
: LENGTH: 1186
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-880-457-3

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	Query Match	95.1%;	Score 194;	DB 107;	Length 1186;	
	Best Local Similarity	100.0%;	Pred. No. 4,2e-57;			
	Matches 194;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
QY	1	CATGAGGCTCATTA	AAGCAGTCTTCTCT	CGGAACAATGACCAAGATTGGCGAAACGTC	60	
Db	504	CATGAGGCTCATTA	AACGACAGTCTTCTCT	CGGAACAATGACCAAGATTGGCGAAACGTC	563	
QY	61	TCCAAACATGACTTC	CAGAACGGAACCAACTAAGAGTCA	AAAGGCAATTTATTACCGGATGCC	120	
Db	564	TCCAAACATGACTTC	CAGAACGGAACCAACTAAGAGTCA	AAAGGCAATTTATTACCGGATGCC	623	
QY	121	GACATTTGCTCTCG	ACATCGCGTAAACCTCAGCAGGCGCT	TAACCTCTGACAGACCTTAGCTA	180	
Db	624	GACATTTGCTCTCG	ACATCGCGTAAACCTCAGCAGGCGCT	TAACCTCTGACAGACCTTAGCTA	683	
QY	181	TGCTGTAAATTTGAG				
Db	684	TGCTGTAAATTTGAG	697			

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RESULT 3
US-09-880-457-2
: Sequence 2, Application US/09880457
: Patent No. US20020106728A1
: GENERAL INFORMATION:
: APPLICANT: Pan, James
: APPLICANT: Goddard, Audrey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
: TITLE OF INVENTION: for the Treatment of Body Weight Disorders
: FILE REFERENCE: P2871A1
: CURRENT APPLICATION NUMBER: US/09/880,457
: CURRENT FILING DATE: 2001-06-12
: PRIOR APPLICATION NUMBER: US 60/212,901
: PRIOR FILING DATE: 2000-06-20
: NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 2
: LENGTH: 2412
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-880-457-2

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Query Match      95.1%  Score 194;  DB 10  Length 2412;
Best Local Similarity 100.0%  Pred. No. 5,66-57;
Matches 194;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0
QY      1  CATGGGCTCATTAACGAGTCCTCTTCGGAACATGACCAAGATTGGGCCAAACGTC 60
      1841 CATGGGCTCATTAACGAGTCCTCTTCCTCTTGGAACATGACCAAGATTGGGCCAAACGTC 1900

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QY	61	TCGACATGACTTTCGACAGGAAACCTAAGAGTCAAAAGCATTTATTACCGGAAATGCC	120
Db	1901	TCGACATGACTTTCGACAGGAAACCTAAGAGTCAAAAGCATTTATTACCGGAAATGCC	1960
QY	121	GACATTGCTCTCGACATCGCTTAACCTGAGCAGGCTTACTCTGCAGACCTTAGCTA	180
Db	1961	GACATTGCTCTCGACATCGCTTAACCTGAGCAGGCTTAACCTCTCAGAGACCTTAGCTA	2020
QY	181	TGGTGTAAATTTGAG	194
Db	2021	TGGTGTAAATTTGAG	2034

RESULT 4
US-09-877-650-12
; Sequence 12, Application US/09877650
; Patent No. US20020169117A1
GENERAL INFORMATION

APPLICANT: Anderson, Dirk M.

Maraskovsky, Eugene

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street

CITY: Seattle
STATE: WA

COUNTRY: USA
ZTP: 98101

COMPUTER READABLE
MEDIUM TYPE.

```

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating

```

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SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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APPLICANT NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001

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CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
```

REGISTRATION NUMBER: 08/995,655
FILING DATE: 1997-12-22

FILING DATE: 07 MARCH 1997

FILING DATE: 23 DECEMBER 1996

NAME: Perkins, Patricia Anne

REFERENCE/DOCKET NUMBER: 2852-A

TELEPHONE: (206) 587-0430

INFORMATION FOR SEQ ID NO: 12:

LENGTH: 954 base pairs

STRANDEDNESS: single

MOLECULE TYPE: cDNA

ANTI-SENSE: NO

ORGANISM: *Homo sapiens*

LIBRARY: <Unknown>

FEATURE: NAME/VIEW: CDD

LOCATION: 1..951

S-09-877-650-12

Downloaded from <http://ajph.org/> on November 10, 2014

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-017-910-1

Query Match 45.7%; Score 93.2; DB 9; Length 1823;
Best Local Similarity 73.4%; Pred. No. 2,3e-22;
Matches 135; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 3 TGAGCCTCATAAAGCAGTCTTCTCTGGAACATGACCAAGATTGGGCAACGCTCTC 62
DB 315 TGGTCCCATAAAGTCACTCTCTCTGTTGTTACCATGATCGGGGGTAAAGATCTC 374
QY 63 CAACATGACTTTCAGCAACGGAACCTAGAGTCA-----AAGCATTTATTACCGGAA 116
DB 375 CACATGACTTTTAGCATGGAACAAATAGTTAATCAGAGATGGCTTTATTACCTGTA 434
QY 117 TGGCAGATTGCTCTGACATGCGCTAACCTAGCAGGCTTCTGACGAGACCTTCA 176
DB 435 TGGCAACATTTGCTTTGACATCATGAACCTCAGAGACCTAGTACAGATATCTTCA 494
QY 177 GCTA 180
DB 495 ACTA 498

RESULT 7

US-09-877-650-10
Sequence 10, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/913,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: RANKL
FEATURE:

NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-877-650-10

Query Match 39.6%; Score 80.8; DB 9; Length 1630;
Best Local Similarity 70.2%; Pred. No. 4e-18;
Matches 125; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 8 CTCATTAACAGAGTCTTCTCTTGTGAAACATGACCAAGATTGGGCAACGCTTCAACA 67
DB 469 CCCATAAAGTCACTCTGCTCTCTTGTGACAGATCGAGGCTGGCCAAAGATCTCTACA 528
QY 68 TGACCTTTCAGCAACGGAACCTAGAGTCA-----AAGCATTTATTACCGGAATGCGG 121
DB 529 TGACCTTTCAGCAACGGAACCTAGAGTCA-----AAGCATTTATTACCGGAATGCGG 121
QY 122 ACATTTGCTCTGACATGCGCTAACCTCAGCAGGCTTCTGACGAGACCTTACGT 179
DB 589 ACATTTGCTCTGACATGCGCTAACCTCAGCAGGCTTCTGACGAGACCTTACGT 646

RESULT 8

US-09-871-856-10
Sequence 10, Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne

RESULT 9
 US-10-017-910-3
 ; Sequence 3, Application US/10017910
 ; Patent No. US20020159970A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Choi, Yongwon
 ; Wong, Brian
 ; Josien, Regis
 ; Steinman, Ralph
 ; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
 ; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME
 ; METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue, 4th Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/017,910
 ; FILING DATE: 14-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/447,035

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RESULT 10
US-09-880-457-9
: Sequence 9, Application US/09880457
: Patent No. US20020106728A1
: GENERAL INFORMATION:
: APPLICANT: Pan, James
: APPLICANT: Goddard, Audrey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
: TITLE OF INVENTION: for the Treatment of Body Weight Disorders
: FILE REFERENCE: P2871R1
: CURRENT APPLICATION NUMBER: US/09/880,457
: PRIOR FILING DATE: 2001-06-12
: PRIOR APPLICATION NUMBER: US 60/212,901
: PRIOR FILING DATE: 2000-06-20
: NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 9
: LENGTH: 61
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Cloning oligonucleotide
US-09-880-457-9

Query Match          29.9%; Score 61; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 6,5e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 CAGCAACGGAAACTAAGACGTCACAAGGACATTATTATCCGGAATGCCGACATTTGCTCTCG 134
|||||
1 CAGCAACGGAAACTAAGACGTCACAAGGACATTATTATCCGGAATGCCGACATTTGCTCTCG 60

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OY 135 A 135
Db 61 A 61

RESULT 11

US-10-040-739-93
; Sequence 93, Application US/10040739
; Patent No. US20020173635A1
; GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

MCCOY, John

Lavallie, Edward

Racie, Lisa

Merberg, David

Treacy, Maurice

Spaulding, Vikki

TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS

NUMBER OF SEQUENCES: 1519

CORRESPONDENCE ADDRESS:

ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/040,739

FILING DATE: 07-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/036,520

FILING DATE: 03-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 93:

SEQUENCE CHARACTERISTICS:

LENGTH: 493 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 93:

US-10-040-739-93

Query Match 15.3%; Score 31.2; DB 9; Length 493;

Best Local Similarity 54.3%; Pred. No. 0.28; Mismatches 53; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 11 ATAAACGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCAACATGA 70

Db 317 AAACAACGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCAACATGA 70

OY 71 CTTTCAGCAAGCAAACTAAGAGTCAAAAGCATTTATTACCGGAATGCCGACATT 126

Db 377 ATTGAATTGTGGGACAGCAAGCATTTATTATGTGAATGGCGAGAAATT 432

RESULT 12

US-09-920-300A-1691

; Sequence 1691, Application US/09920300A

; Patent No. US20020136728A1

; GENERAL INFORMATION:

APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Xu, Jianshun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1691

LENGTH: 985

TYPE: DNA

ORGANISM: Homo sapiens

US-09-920-300A-1691

Query Match 15.3%; Score 31.2; DB 10; Length 985;

Best Local Similarity 54.3%; Pred. No. 0.37; Mismatches 53; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 11 ATAAACGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCAACATGA 70

Db 387 AAACAACGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCAACATGA 70

OY 71 CTTTCAGCAAGCAAACTAAGAGTCAAAAGCATTTATTACCGGAATGCCGACATT 126

Db 447 ATTGAATTGTGGGACAGCAAGCATTTATTATGTGAATGGCGAGAAATT 502

RESULT 13

US-10-033-528-1691

; Sequence 1691, Application US/10033528

; Patent No. US2002013971A1

; GENERAL INFORMATION:

APPLICANT: King, Gordon E.

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Xu, Jianshun

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.547C1

CURRENT APPLICATION NUMBER: US/10/033,528

CURRENT FILING DATE: 2001-12-26

NUMBER OF SEQ ID NOS: 1896

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1691

LENGTH: 985

TYPE: DNA

ORGANISM: Homo sapiens

US-10-033-528-1691

Query Match 15.3%; Score 31.2; DB 12; Length 985;

Best Local Similarity 54.3%; Pred. No. 0.37; Mismatches 53; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

OY 11 ATAAACGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCAACATGA 70

Db 387 AAACAACGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGTCCTCAACATGA 70

OY 71 CTTTCAGCAAGCAAACTAAGAGTCAAAAGCATTTATTACCGGAATGCCGACATT 126

Db 447 ATTGAATTGTGGGACAGCAAGCATTTATTATGTGAATGGCGAGAAATT 502

RESULT 14

US-09-867-701-10910

; Sequence 10910, Application US/09867701

; Patent No. US20020132237A1

; GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

```

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAP
:
: FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: TITLE REFERENCE: 210121.497
:
: CURRENT APPLICATION NUMBER: US/09/867,701
:
: CURRENT FILING DATE: 2001-05-29
:
: NUMBER OF SEQ ID NOS: 10912
:
: SOFTWARE: FASTSEQ for Windows Version 4.0
:
: SEQ ID NO 10910
:
: LENGTH: 3073
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-867-701-10910

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Query Match	15.38;	Score 31.2;	DB 10;	Length 3073;
Best Local Similarity	54.38;	Pred. No. 0.6;		
Matches	63;	Conservative	0;	Mismatches 53;
			Indels	0;
			Gaps	0

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US-09-920-300A-1690
RESULT 15
US-09-920-300A-1690
Sequence 1690, Application US/099203000A
Patent No. US20020136728A1
GENERAL INFORMATION:
APPLICANT: King, Gordon F.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS
OF TITRATION AND DIAGNOSIS OF COLIC
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FASTSEQ For Windows Version 4.0
SEQ ID NO. 1690
LENGTH: 3073
TYPE: DNA
ORGANISM: Homo sapiens
US-09-920-300A-1690

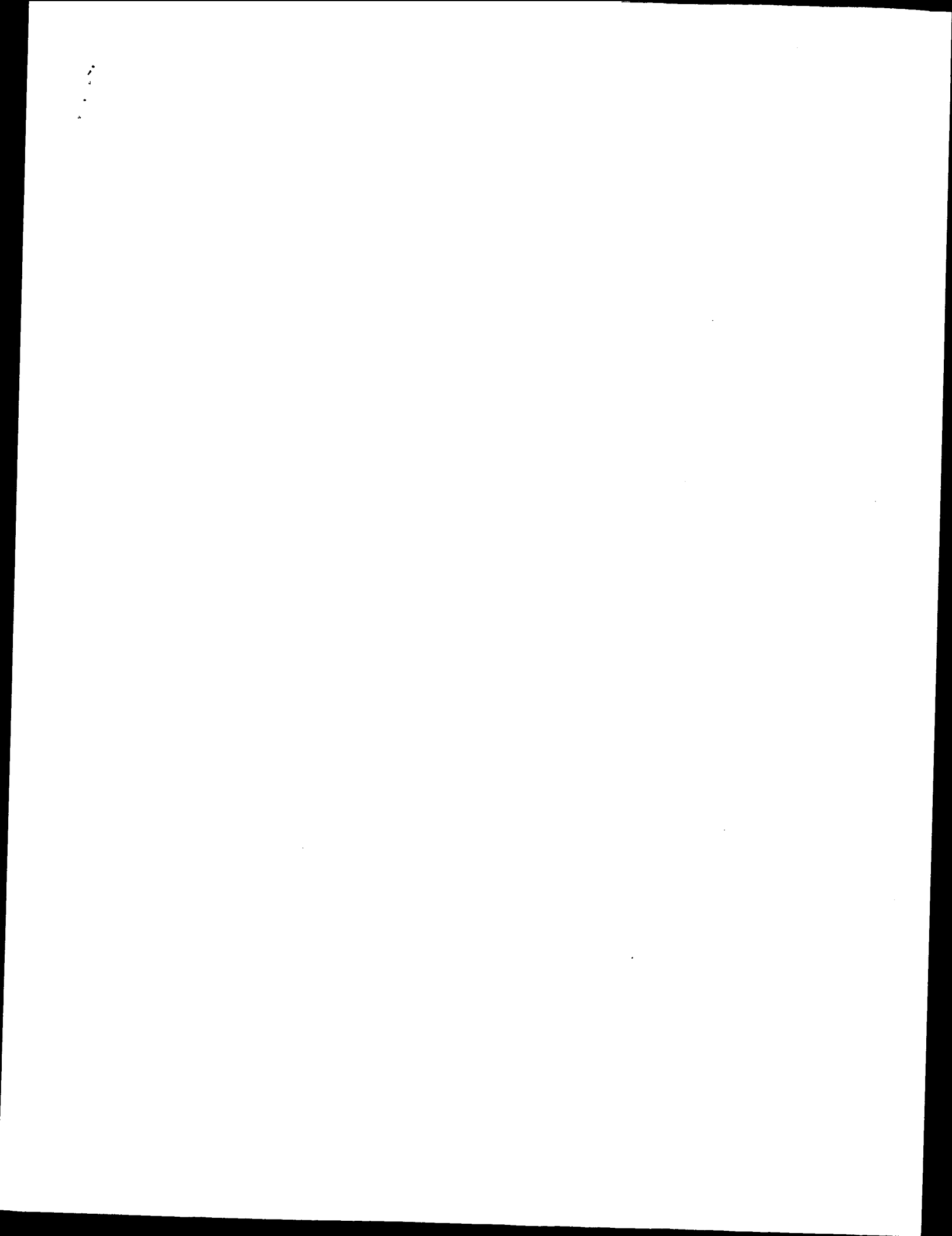
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Query Match	15.3%	Score 31.2;	DB 10;	Length 3073;
Best Local Similarity	54.3%	Pred. No. 0.6;		
Matches	63;	Conservative	0;	Mismatches 53;
			Indels	0;
			Gaps	0;

[illegible]

07 71 CTTTCAGCAACGGAAAACTAGAGTCAAGGACATTTATTACCGGAATCCGACATC 126
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 Db 1330 ATTGAATTTGGGACACGACACATTTAAAGGACATTTATGCTGAATGGCAGACAAATT 1385

Search completed: December 8, 2002, 19:38:04
Job time : 18.9188 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:18:27 ; Search time 15.2491 Seconds
(without alignments)
6674.007 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atggcaatcctgacgctcag.....gttaattgagaatcattcag 261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Published Applications, NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCIT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCITUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	261	100.0	1161	10	US-09-880-457-1 Sequence 1, Appl1
2	251	96.2	1186	10	US-09-880-457-3 Sequence 3, Appl1
3	249.4	95.6	2412	10	US-09-880-457-2 Sequence 2, Appl1
4	121.2	46.4	954	9	US-09-877-650-12 Sequence 12, Appl1
5	121.2	46.4	954	10	US-09-871-856-12 Sequence 12, Appl1
6	118	45.2	1823	9	US-09-877-650-10 Sequence 1, Appl1
7	95.6	36.6	1630	9	US-09-871-856-10 Sequence 1, Appl1
8	95.6	36.6	1630	10	US-09-871-856-10 Sequence 1, Appl1
9	95.6	36.6	2237	9	US-10-017-910-3 Sequence 3, Appl1
10	61	23.4	61	10	US-09-880-457-9 Sequence 9, Appl1
11	33	12.6	454	10	US-09-864-761-14164 Sequence 14164, A
12	31.2	12.0	493	9	US-10-040-739-93 Sequence 93, Appl1
13	31.2	12.0	985	10	US-09-920-300A-1691 Sequence 1691, Ap
14	31.2	12.0	985	12	US-10-033-528-1691 Sequence 1691, Ap
15	31.2	12.0	3073	10	US-09-867-701-10910 Sequence 10910, A
16	31.2	12.0	3073	10	US-09-920-300A-1690 Sequence 1690, Ap
17	31.2	12.0	3073	12	US-10-033-528-1690 Sequence 1690, Ap
18	30.8	11.6	30310	10	US-09-800-631-96 Sequence 96, Appl1
19	30.4	11.6	53226	10	US-09-818-264-3 Sequence 3, Appl1

C 20	30.2	11.6	2000	10	US-09-887-576-151	Sequence 151, App
C 21	30	11.5	30	10	US-09-880-457-8	Sequence 8, Appl1
C 22	29.6	11.3	2048	10	US-09-764-847-1468	Sequence 1468, App
C 23	29.4	11.3	409	10	US-09-783-590-1953	Sequence 1953, App
C 24	29.4	11.3	2244	10	US-09-764-864-153	Sequence 153, App
C 25	28.8	11.0	257	10	US-09-878-574-7063	Sequence 7063, App
C 26	28.8	11.0	143068	10	US-09-967-768A-316	Sequence 316, App
C 27	28.6	11.0	357	10	US-09-878-574-3028	Sequence 3028, App
C 28	28.6	11.0	407	10	US-09-878-574-3146	Sequence 3146, App
C 29	28.6	11.0	1365	10	US-09-815-242-4243	Sequence 4243, App
C 30	28.6	11.0	1365	10	US-09-815-242-8196	Sequence 8196, App
C 31	28.2	10.8	477	10	US-09-759-143-92	Sequence 92, Appl1
C 32	28.2	10.8	477	10	US-09-780-669-92	Sequence 92, Appl1
C 33	28.2	10.8	477	10	US-09-030-606-92	Sequence 92, Appl1
C 34	28.2	10.8	477	10	US-09-822-827-92	Sequence 92, Appl1
C 35	28.2	10.8	477	10	US-09-115-453-92	Sequence 92, Appl1
C 36	28.2	10.8	2000	9	US-09-938-842A-4251	Sequence 4251, App
C 37	28	10.7	398	10	US-09-983-965-5848	Sequence 5848, App
C 38	28	10.7	932	10	US-09-925-300-515	Sequence 515, App
C 39	27.8	10.7	666	10	US-09-764-864-590	Sequence 590, App
C 40	27.8	10.7	2147	9	US-09-981-353-104	Sequence 104, App
C 41	27.8	10.7	2222	9	US-09-981-353-76	Sequence 76, Appl1
C 42	27.8	10.7	465237	10	US-09-933-267A-1	Sequence 1, Appl1
C 43	27.6	10.6	371	10	US-09-834-975-285	Sequence 285, App
C 44	27.6	10.6	486	10	US-09-783-590-10438	Sequence 10438, A
C 45	27.6	10.6	608	10	US-09-759-143-193	Sequence 193, App

ALIGNMENTS

RESULT 1
US-09-880-457-1
Sequence 1, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P287191
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-1

Query Match 100.0%; Score 261; DB 10; Length 1161;
Best Local Similarity 100.0%; Pred. No. 1.6e-77;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCAATCCTGACGCTGACGCTTCAATCATCTGTTATTAATACCATCAATATCCAT	60
DB	486	ATGGCAATCCTGACGCTGACGCTTCAATCATCTGTTATTAATACCATCAATATCCAT	545
QY	61	GAGGCTATAAAGCATCTCTCTTGGAAACATGACCAATGGGCAACGCTCC	120
DB	546	GAGGCTATAAAGCATCTCTCTTGGAAACATGACCAATGGGCAACGCTCC	605
QY	121	AACATGACTTTCAGACGGAAGAACTAAGATCAAGGATTTATTAACCGAATGCCGAC	180
DB	606	AACATGACTTTCAGACGGAAGAACTAAGATCAAGGATTTATTAACCGAATGCCGAC	665
QY	181	ATTGCTCTGACATTCGCGTACCTGACGAGGCTTAATCTGACGAGCCTTCGATGG	240
DB	666	ATTGCTCTGACATTCGCGTACCTGACGAGGCTTAATCTGACGAGCCTTCGATGG	725

QY 241 TGTAAATTTGAGATCATTCAC 261
Db 726 TGTAAATTTGAGATCATTCAC 746

RESULT 2

US-09-880-457-3
; Sequence 3, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-3

Query Match 96.2%; Score 251; DB 10; Length 1186;
Best Local Similarity 100.0%; Pred. No. 3 6e-74;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAATCCCTGAGCGCTCAGCTTCAACTCATCTGTTATTATATACCATCAATATCCCAT 60
Db 447 ATGGCAATCCCTGAGCGCTCAGCTTCAACTCATCTGTTATTATATACCATCAATATCCCAT 506
QY 61 GAGGCTCATATAAAGAGATCTTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 120
Db 507 GAGGCTCATATAAAGAGATCTTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 566
QY 121 AACATGACTTTCAGCAACGAGAACTAAGATCAAGGCAATTTATACCGGAATGCCGAC 180
Db 567 AACATGACTTTCAGCAACGAGAACTAAGATCAAGGCAATTTATACCGGAATGCCGAC 626
QY 181 ATTTGCTCTGACATCGCGTAACCTCAGACGCTTAACCTCGACGACCTTCAGCTATGG 240
Db 627 ATTTGCTCTGACATCGCGTAACCTCAGACGCTTAACCTCGACGACCTTCAGCTATGG 686
QY 241 TGTAAATTTGAG 251
Db 687 TGTAAATTTGAG 697

RESULT 3

US-09-880-457-2
; Sequence 2, Application US/09880457
; Patent No. US20020106728A1
; GENERAL INFORMATION:
; APPLICANT: Pan, James
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
; FILE REFERENCE: P2871R1
; CURRENT APPLICATION NUMBER: US/09/880,457
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 60/212,901
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-880-457-2

Query Match 95.6%; Score 249.4; DB 10; Length 2412;
Best Local Similarity 99.6%; Pred. No. 1.7e-73;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAATCCCTGAGCGCTCAGCTTCAACTCATCTGTTATTATATACCATCAATATCCCAT 60
Db 1784 ATGGCAATCCCTGAGCGCTCAGCTTCAACTCATCTGTTATTATATACCATCAATATCCCAT 1843
QY 61 GAGGCTCATATAAAGAGATCTTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 120
Db 1844 GAGGCTCATATAAAGAGATCTTTCTTCTTGGAAACATACCAAGATTTGGCAACGCTCTCC 1903
QY 121 AACATGACTTTCAGCAACGAGAACTAAGATCAAGGCAATTTATACCGGAATGCCGAC 180
Db 1904 AACATGACTTTCAGCAACGAGAACTAAGATCAAGGCAATTTATACCGGAATGCCGAC 1963
QY 181 ATTTGCTCTGACATCGCGTAACCTCAGACGCTTAACCTCGACGACCTTCAGCTATGG 240
Db 1964 ATTTGCTCTGACATCGCGTAACCTCAGACGCTTAACCTCGACGACCTTCAGCTATGG 2023
QY 241 TGTAAATTTGAG 251
Db 2024 TGTAAATTTGAG 2034

RESULT 4

US-09-877-650-12
; Sequence 12, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation, Law Department

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/877,650

FILING DATE: 08-Jun-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 954 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-877-650-12

Query Match 46.4%; Score 121.2; DB 9; Length 954;
Best Local Similarity 74.8%; Pred. No. 7.2e-31;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCTGAGCGTCAGCCTTCACTCATCTTGTATTATATCAATATCCCATGAG 63
DB 473 GCAGCTTGAGCTGAGCCTTTTGGCTCATCTATTAATGCCACCATCCCATCTG 532
QY 64 GCT--CATAAACGAGCTCTTCTCTGGAACATGACCAAGATGGGCAACGCTCCA 121
DB 533 GTTCCCATTAAGTAGCTGTCTCTTGTGATGATGCGGCTTGGGCAAGATCTCCA 592
QY 122 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 652
QY 176 CCGAGATTTGCTCGACATCGCGTAACTCAGCAGGCTTACCTGCGAGGACTTCAGC 235
DB 653 CCAACATTTGCTTTCGACATCATGAACCTTCAGAGAGCTTACGATGATCTTCAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 5

US-09-871-856-12
Sequence 12, Application US/09871856
Patent No. US20020081720A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/871.856

FILING DATE: 31-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139

FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0450
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 954 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

LIBRARY: <Unknown>

CLONE: hURANKL (full length)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..951

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-871-856-12

Query Match 46.4%; Score 121.2; DB 10; Length 954;
Best Local Similarity 74.8%; Pred. No. 7.2e-31;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCTGAGCGTCAGCCTTCACTCATCTTGTATTATATCAATATCCCATGAG 63
DB 473 GCAGCTTGAGCTGAGCCTTTTGGCTCATCTATTAATGCCACCATCCCATCTG 532
QY 64 GCT--CATAAACGAGCTCTTCTCTGGAACATGACCAAGATGGGCAACGCTCCA 121
DB 533 GTTCCCATTAAGTAGCTGTCTCTTGTGATGATGCGGCTTGGGCAAGATCTCCA 592
QY 122 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTCAGCAGGAAACTAGAGTCA-----AAGCATTTATTACCGGAATG 652
QY 176 CCGAGATTTGCTCGACATCGCGTAACTCAGCAGGCTTACCTGCGAGGACTTCAGC 235
DB 653 CCAACATTTGCTTTCGACATCATGAACCTTCAGAGAGCTTACGATGATCTTCAC 712
QY 236 TA 237
DB 713 TA 714

RESULT 6

US-10-017-910-1
Sequence 1, Application US/10017910
Patent No. US2002015970A1

GENERAL INFORMATION:

APPLICANT: Choi, Yongwon

Wong, Brian

Josien, Ralph

Steinman, Ralph

TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY

INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING

METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/017,910
FILING DATE: 14-Dec-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq. David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1823 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..738
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-017-910-1

Query Match
Best Local Similarity 45.2%; Score 118; DB 9; Length 1823;
Matches 179; Conservative 0; Mismatches 55; Indels 8; Gaps 2;

QY 4 GCAATTCGAGCTGAGCTTCAACATCTGTATTATATCAATATATCCATAG 63
DB 257 GCAAGCTTGAAGCTGCTTTTGTCTCACTCACTATTAATGACCGCATCCCATCTG 316
QY 64 GGT--CATAAACGAGCTCTTCTTGTGAAACATGACCAAGATGGGCAACGCTCTCA 121
DB 317 GTTCCCATTAAGTGAAGTGTCTCTCTGTACATGATGGGGGTGGGTAAGATCTTCA 376
QY 122 ACATGACTTTCAGCAACGAAACCTAAGATCA-----AAGCATTTATTACCGGAATG 175
DB 377 ACATGACTTTTACGAAATGAAACTAATAGTTATCAGATGGCTTTTATTACCTGTATG 436
QY 176 CCGAATTTGCTCTGACATGCGCTAACCTCAGCAGCGCTTAAGTCTGAGGAGACCTTACG 235
DB 437 CCAACATTTGCTTTCGACATCATGAAGCTTACGAGAGACCTTACGAGATATCTTCAAC 496
QY 236 TA 237
DB 497 TA 498

RESULT 7
US-09-877-650-10
Sequence 10, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY: <unknown>
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-877-650-10

Query Match
Best Local Similarity 36.6%; Score 95.6; DB 9; Length 1630;
Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps 2;

QY 3 GGCATCTGAGCTGAGCTTCAACATCTGTATTATTAATACATCAATATCCATGA 62
DB 405 GGCAGCCTGAGGCCGACCATTTGACACCTTCACCATCAATGTCGACGATGCCATG 464
QY 63 GG--CTCATAAACGAGCTTCTTCTTGAACATGACCAAGATTTGGCAACGCTTCC 120
DB 465 GGTTCCTCATTAAGTACTGTCTCTGTACACGATCGAGCTGGGCAAGATCTCT 524
QY 121 AACATGACTTTCAGCAACGAAACTAAGATCA-----AAGCATTTATTACCGGAAT 174
DB 525 AACATGACCTTAAGCAAGGAAACTAAGGTTTACCAAGATGGCTTCTTATTACCTGTAG 584
QY 175 GCCGACATTTGCTCTGACATGCGCTAACCTCAGCAGCGCTTAAGTCTGAGGAGACCTTACG 234
DB 585 GCCAACATTTGCTTTCGACATCATGAAGCTTACGAGAGCTTACGAGACTATCTTACG 644
QY 235 CT 236
DB 645 CT 646

RESULT 8
US-09-871-856-10
Sequence 10, Application US/09871856

```

1 Patent No. US20020081720A1
2 GENERAL INFORMATION:
3 APPLICANT: Anderson, Dirk M.
4 Galibert, Laurent
5 Markaskovsky, Eugene
6 TITLE OF INVENTION: Receptor Activator of NF-kappaB
7 NUMBER OF SEQUENCES: 19
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Immunex Corporation, Law Department
10 STREET: 51 University Street
11 CITY: Seattle
12 STATE: WA
13 COUNTRY: USA
14 ZIP: 98101
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: Apple Power Macintosh
19 OPERATING SYSTEM: Apple Operating System 7.5.5
20 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/871,856
23 FILING DATE: 31-May-2001
24 CLASSIFICATION: <Unknown>
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/996,139
28 FILING DATE: <Unknown>
29 APPLICATION NUMBER: USSN 08/813,509
30 FILING DATE: 07 MARCH 1997
31 APPLICATION NUMBER: USSN 08/772,330
32 FILING DATE: 23 DECEMBER 1996
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Perkins, Patricia Anne
35 REGISTRATION NUMBER: 34,693
36 REFERENCE/DOCKET NUMBER: 2851-A
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (206)587-0430
39 TELEFAX: (206)233-0644
40
41 INFORMATION FOR SEQ ID NO: 10:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 1630 base pairs
44 TYPE: nucleic acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 MOLECULE TYPE: cDNA
48 HYPOTHEetical: NO
49 ANTI-SENSE: NO
50 ORIGINAL SOURCE:
51 ORGANISM: Mus musculus
52 IMMEDIATE SOURCE:
53 LIBRARY: <Unknown>
54 CLONE: RANKL
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: 3..884
58
59 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
60 US-09-871-856-10
61
62 Query Match 36.6%; Score 95.6; DB 10; Length 1630;
63 Best Local Similarity 68.2%; Pred. No.3.2e-22;
64 Matches 165; Conservative 0; Mismatches 69; Indels 8; Gaps
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[illegible]

OY		63	GG-CTCATTAAGAAGACTTTTCTTCGTGGAAACATACCAGAATTGGGAACAAGCTCC	120
Dd		670	GTTTTCCATAAAGTCACCTCTCCTCTTGCGAACGCATCGAGGCGTGGGCCAAGATCTCF	729
OY		121	AACATGACTTTCAGCAACGAAAACTAAGAGTCA-----AAGGCATTATTACCGGAAT	174
Dd		730	AACATGAGCTTAACCAACGSAANAACCTAAGGGTTAACCAAGTAGGCTCTATTACCTGTAC	789
OY		175	GCCGACATTTCCTCTCCACATCGCGTAACTCCACACAGGCTTAACCTTCGACAGGACTTCAG	234
Dd		790	GCCAACTATTTCCTTCGCGATCATGAAGAACATCGGGAAGCGCTACTACAGACTATCTTCAG	849
OY		235	CT 236	
Dd		850	CT 851	

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: RESULT 10
: US-09-880-457-9
: Sequence 9, Application US/09880457
: Patent No. US20020106728A1
: GENERAL INFORMATION:
: APPLICANT: Pan, James
: APPLICANT: Goddard, Audrey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: N54 Nucleic Acids and Peptides and Methods of Use
: TITLE OF INVENTION: for the Treatment of Body Weight Disorders
: FILE REFERENCE: P2871r1
: CURRENT APPLICATION NUMBER: US/09/880,457
: CURRENT FILING DATE: 2001-06-12
: PRIOR APPLICATION NUMBER: US 60/212,901
: PRIOR FILING DATE: 2000-06-20
: NUMBER OF SEQ ID NOS: 9
: SEQ ID NO 9
: LENGTH: 61
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Cloning oligonucleotide
: US-09-880-457-9

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	Query Match	23.4%	Score 61:	DB 10;	Length 61:	
	Best Local Similarity	100.0%	Pred. No.	2.7-11;		
Matches	61:	Conservative	0:	Mismatches	0:	Indels
					0:	Gaps
QY	132	CAGCAGCGAAACCTAAGCATTCGCAATCCGATCCGCAGATTGGCTCTCG	191			
Dd	1	CAGCAGCGAAACCTAAGCATTCGCAATCCGATCCGCAGATTGGCTCTCG	60			
QY	192	A	192			
Dd	61	A	61			

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, RESULT 11
, US-09-864-761-14164/C
, Sequence 14164, Application US/09864761
, Patent NO. US20020048763A1
, GENERAL INFORMATION:
, APPLICANT: Penn, Sharon G.
, APPLICANT: Rank, David R.
, APPLICANT: Hanzel, David K.
, APPLICANT: Chen, Wensheng
, TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
, TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
, FILE REFERENCE: Aemica-X-1
, CURRENT APPLICATION NUMBER: US/09/864,761
, CURRENT FILING DATE: 2001-05-23
, PRIOR APPLICATION NUMBER: US 60/180,312
, PRIOR FILING DATE: 2000-02-04
, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 09/632,366

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1  PRIOR FILING DATE: 2000-08-03
2  PRIOR APPLICATION NUMBER: GB 24263. 6
3  PRIOR FILING DATE: 2000-10-04
4  PRIOR APPLICATION NUMBER: US 60/236, 359
5  PRIOR FILING DATE: 2000-09-27
6  PRIOR APPLICATION NUMBER: PCT/US01/00666
7  PRIOR FILING DATE: 2001-01-30
8  PRIOR APPLICATION NUMBER: PCT/US01/00667
9  PRIOR FILING DATE: 2001-01-30
10 PRIOR APPLICATION NUMBER: PCT/US01/00664
11 PRIOR FILING DATE: 2001-01-30
12 PRIOR APPLICATION NUMBER: PCT/US01/00669
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: PCT/US01/00665
15 PRIOR FILING DATE: 2001-01-30
16 PRIOR APPLICATION NUMBER: PCT/US01/00668
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/00663
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/00662
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/00661
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00670
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: US 60/234, 687
27 PRIOR FILING DATE: 2000-09-21
28 PRIOR APPLICATION NUMBER: US 09/608, 408
29 PRIOR FILING DATE: 2000-06-30
30 PRIOR APPLICATION NUMBER: US 09/774, 203
31 PRIOR FILING DATE: 2001-01-29
32 NUMBER OF SEQ ID NOS: 49117
33 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
34 SEQ ID NO 14164
35 LENGTH: 454
36 TYPE: DNA
37 ORGANISM: Homo sapiens
38 FEATURE:
39 OTHER INFORMATION: MAP TO AL021307.1
40 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
41 US-09-864-761-14164

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	Query Match	Best Local Similarity	Matches	12.6%	Score 33;	DB 10;	Length 454;
				50.3%;	Pred. No. 0.15;		
				Conservative	0;	Mismatches 80;	Indels 0; Gaps 0.
QY	41	TAATACCATCAATATTCACATGAGGCTCATATAACGAGTCTTTCTTCTTGGAACAATGACC	100				
DB	429	TGATACCTGTTTTTTCACCTATTATAGCGTGACAAATGTTTACTATTTTTGCTACATACATGGCT	370				
QY	101	AAGATTGGGCAACGCTCTCCACATGACTTTTAGCAACGGAACCTAGAGTCACAAAGCA	160				
DB	369	GAGATTGTGGAGGCAAAATACATTCACACAACTGCTGTGGGAACAATATATGATATTTT	310				
QY	161	TTTATTACCGGAATGCCGACATTTTGCTCTCGCATCGCGCTA	201				
DB	309	TCTGTAATTAATAATACGGCATTTATCTACCAAAATTTAGCTA	269				

RESULT 12 739-93
US-10-040-739-93
: Sequence 93, Application US/10040739
: Patent No. US20020173635A1
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: McCoy, John
: LaVallie, Edward
: Racle, Lisa
: Merberg, David
: Treacy, Maurice
: Spaulding, Vikki
: TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
: NUMBER OF SEQUENCES: 1519
:

QY 128 CTTTCAGCAACGAAACTAGAGTCACAAGCATTTATTACCGAATGCCGACATT 183
|||
Db 1330 ATTGAATTGTGGACACGACATTCACAAGGCATTTATGCTGATGGCGCAGAAATT 1385

Search completed: December 8, 2002, 19:37:57
Job time : 24.2491 secs

Tue Dec 10 10:51:28 2002

us-09-880-457-1.rnpb

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:18:27 ; Search time 67.8321 Seconds
(without alignments)
6674.007 Million cell updates/sec

Title: US-09-880-457-1

Perfect score: 1161
Sequence: 1 aaaaagagataatcaaga.....taataaagagagaatgc 1161

Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/pubpna/US06_PUB_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_PUB_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_PUB_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US09_PUB_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US10_PUB_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US60_PUB_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1161	100.0	1161	10	US-09-880-457-1
2	412	35.5	2412	10	US-09-880-457-2
3	268	23.1	1186	10	US-09-880-457-3
4	126	10.9	954	9	US-09-877-650-12
5	126	10.9	954	10	US-09-871-856-12
6	122.8	10.6	1823	9	US-10-017-910-1
7	97	8.4	1630	9	US-09-877-650-10
8	97	8.4	1630	10	US-09-871-856-10
9	97	8.4	2237	9	US-10-017-910-3
10	61	5.3	61	10	US-09-880-457-9
11	38	3.3	180216	10	US-09-835-232-6
12	38	3.3	197997	10	US-09-822-246-3
13	35.6	3.1	370	10	US-09-867-701-6187
14	35.6	3.1	495	10	US-09-867-701-10680
15	35.2	3.0	12259	10	US-09-764-869-1690
16	34.2	2.9	606	10	US-09-918-686-9
17	34.2	2.9	51719	10	US-09-918-686-2
18	34.2	2.9	92139	10	US-09-918-686-1
19	33.8	2.9	17761	10	US-09-764-847-1596

20	33.6	2.9	147309	10	US-09-742-312-3	Sequence 3, Appl1
21	33.4	2.9	465237	10	US-09-933-267A-1	Sequence 1, Appl1
22	33.2	2.9	493	10	US-09-864-761-14364	Sequence 14364, A
23	33	2.8	454	10	US-09-864-761-14164	Sequence 14164, A
24	33	2.8	4810	10	US-09-764-869-1995	Sequence 1995, Ap
25	32.8	2.8	14485	10	US-09-876-216-3	Sequence 1673, Ap
26	32.8	2.8	23071	10	US-09-764-864-1673	Sequence 646, App
27	32.6	2.8	385	10	US-09-070-927A-646	Sequence 267, App
28	32.4	2.8	407	10	US-09-764-869-267	Sequence 4893, Ap
29	32.4	2.8	555	10	US-09-783-590-4893	Sequence 15062, A
30	32.4	2.8	474	10	US-09-864-761-15062	Sequence 3185, Ap
31	32.4	2.8	529	10	US-09-783-590-3185	Sequence 3727, Ap
32	32.4	2.8	22786	10	US-09-841-877-3727	Sequence 3, Appl1
33	32.2	2.8	174493	10	US-09-804-471A-3	Sequence 12, Appl1
34	31.8	2.7	1371	12	US-10-002-600-12	Sequence 1, Appl1
35	31.6	2.7	456	10	US-09-733-523-1	Sequence 245, App
36	31.6	2.7	521	9	US-09-924-400-245	Sequence 245, App
37	31.6	2.7	521	10	US-09-810-936-245	Sequence 245, App
38	31.6	2.7	521	10	US-09-429-75A-245	Sequence 595, App
39	31.4	2.7	900	10	US-09-841-132-595	Sequence 440, App
40	31.4	2.7	2172	10	US-09-822-830A-440	Sequence 469, App
41	31.4	2.7	8045	10	US-09-764-887-469	Sequence 292, App
42	31.4	2.7	43058	10	US-09-954-456-292	Sequence 529, App
43	31.4	2.7	43058	10	US-09-954-456-529	Sequence 3950, Ap
44	31.4	2.7	43058	10	US-09-880-107-3950	Sequence 442, App
45	31.2	2.7	401	9	US-09-946-807-442	

ALIGNMENTS

RESULT 1
US-09-880-457-1
Sequence 1, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Nucleic Acids and Polypeptides and Methods of Use
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-1

Query Match	Score 1161;	DB 10;	Length 1161;
Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches 0;
Matches 1161;	Conservative 0;	Indels 0;	Gaps 0;
1	AAAAGAGATATTCAGAGAGGCTTTAAAGGACTATTTCCCAAGATGGAGATGAG 60		
1	AAAAGAGATATTCAGAGAGGCTTTAAAGGACTATTTCCCAAGATGGAGATGAG 60		
1	AAAAGAGATATTCAGAGAGGCTTTAAAGGACTATTTCCCAAGATGGAGATGAG 60		
61	GGGAACTGCGAGGCTGATGCTTACCTCAGAGGAGGAGGAGGAGGAGGAT 120		
61	GGGAACTGCGAGGCTGATGCTTACCTCAGAGGAGGAGGAGGAGGAGGAGGAT 120		
61	GGGAACTGCGAGGCTGATGCTTACCTCAGAGGAGGAGGAGGAGGAGGAGGAT 120		
121	AAGGACGCTGCTTGCAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 180		
121	AAGGACGCTGCTTGCAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 180		
121	AAGGACGCTGCTTGCAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 180		
181	GGAACACCTGCTTGCAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 240		
181	GGAACACCTGCTTGCAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 240		
181	GGAACACCTGCTTGCAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 240		

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? TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides of Use
?
? TITLE OF INVENTION: for the Treatment of Body Weight Disorders
? FILE REFERENCE: P287JRI
? CURRENT APPLICATION NUMBER: US/09/880,457
? PRIOR FILING DATE: 2001-06-12
? PRIOR APPLICATION NUMBER: US 60/212,901
? PRIOR FILING DATE: 2000-06-20
? NUMBER OF SEQ ID NOS: 9
? SEQ ID NO 2
?
? LENGTH: 2412
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? US-09-880-457-2

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Query Match	35.5%	Score 412;	DB 10;	Length 2412;
Best Local Similarity	73.8%;	Pred. No. 1.4e-122;		
Matches 561; Conservative	0;	Mismatches 175;		

QY 1 AAAAGGGAATTAATTCAGAGAGGCGCTTCTTTAAGGACATATTCCCAAGATGGGAATGAG 60
 Db 1275 AAAAGGGAATTAATTCAGAGAGGCGCTTCTTTAAGGACATATTCCCAAGATGGGAATGAG 1334
 QY 61 GGAACCTTCAGAGGCTAGTGTCTACCTCCAGAGGACACACTTAATCTGAGGGAT 120
 Db 1335 GGAACCTTCAGAGGCTAGTGTCTACCTCCAGAGGACACACTTAATCTGAGGGAT 1394
 QY 121 AAGGACGCGGTTCGAGAGACATGGAGGGAAAGTTCTACAGAGGAGCGACAGGGCTTCA 180
 Db 1395 AAGGACGCGGTTCGAGAGACATGGAGGGAAAGTTCTACAGAGGAGCGACAGGGCTTCA 1454
 QY 181 GGAACACCTGCTTGGAGAGCGCTGTGAGAG--TGGGGAATCAATACCTGACCTCGCT 238
 Db 1455 GGAACACCTGCTTGGAGAGCGCTGTGAGAGGATTTTCTTCTACGTTTTCATTCACGT 1514
 QY 239 CCTTCATCTCTCCCAACCCACAGGCGTTGGTGGGCCCCACAGGCGACCTCCGGG 298
 Db 1515 AACCTCTAACCGTCTCTGGGGAAAGTGTACCCCTCGCTCCCGCTTCCCTGCACT 1574
 QY 289 GAGGAAGTGGAGAGAGGACCTGGAGGCGCATTAAGATGTGACACACAGTATCTCA 358
 Db 1575 CTCTGCAATGGATGGGCTGACTGATGCCCTGGGCTGGAACTGACACAGTTCCTG 1634
 QY 359 GGCACCGGATTTTGTGACATTTGGGATTTGTGACAAACAAAGTCAGACAAAAAAGCT 418
 Db 1635 CAGACGAGACCCCTCTACATAGTGAATGCTGGCTGAGAGATCCAGAGAGCCCGAGGG 1694
 QY 419 TGTCTGTGGAGGAAACATTGTACAAAGGAAGGCAAAATGACAAG----- 465
 Db 1695 GGAACATGAAGTGTATCGTTGGCCCTCCAGCTGCAAGTAAGTGTCTGATGATTT 1754
 QY 466 -----AGGAGAGATTTTGTCAAGAAATGGCAATCCGAGCGCTAGCGTTCAACTCA 516
 Db 1755 TAAAGGAGGAAGAAGATTTTGTCTAAGAAATGGCAATCCGAGCGCTAGCGTTCAACTCA 1814
 QY 517 TCTTGTATTAATACATCAATATCCCATAGGCGTATAAAGAGATCTTTCTTGG 576
 Db 1815 TCTTGTATTAATACATCAATATCCCATAGGCGTATAAAGAGATCTTTCTTGG 1874
 QY 577 AACATGACCAAGATTGGGCAAAAGCTGCCAAATGACTTTCAGCAAGGAAACTTAAG 636
 Db 1875 AACATGACCAAGATTGGGCAAAAGCTGCCAAATGACTTTCAGCAAGGAAACTTAAG 1934
 QY 637 TCAAGGATTTATTAACCGAATGCCGACATTTGCTCTGACATGGCTTAACCTCAGAG 696
 Db 1935 TCAAGGATTTATTAACCGAATGCCGACATTTGCTCTGACATGGCTTAACCTCAGAG 1994
 QY 697 GCCTAATCTGCAGAGCTTCACTGATGTTGGTGTAAATTTGAG 736
 Db 1995 GCCTAATCTGCAGAGCTTCACTGATGTTGGTGTAAATTTGAG 2034

RESULT 3
US-09-880-457-3

Sequence 3, Application US/09880457
Patent No. US20020106728A1
GENERAL INFORMATION:
APPLICANT: Pan, James
APPLICANT: Goddard, Audrey
APPLICANT: Wood, William I.
TITLE OF INVENTION: NS4 Nucleic Acids and Polypeptides and Methods of Use
TITLE OF INVENTION: for the Treatment of Body Weight Disorders
FILE REFERENCE: P2871R1
CURRENT APPLICATION NUMBER: US/09/880,457
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: US 60/212,901
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO: 3
LENGTH: 1186
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-457-3

Query Match 23.1%, Score 268; DB 10; Length 1186;
Best Local Similarity 100.0%; Pred. No. 3.1e-76;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAGATTATTGCTAAGATGCAATCCGAGCGCTCAGCCTTCAACTGATCTGTATTAA 528
DB 430 AGAGATTATTGCTAAGATGCAATCCGAGCGCTCAGCCTTCAACTGATCTGTATTAA 489
QY 529 TACCATCATATCCATGAGGCTCATAAACGAGTCTTCTTCTGGAACATGACCAAG 588
DB 490 TACCATCATATCCATGAGGCTCATAAACGAGTCTTCTTCTGGAACATGACCAAG 549
QY 589 ATTGGGCAAGCTCTCCAAATGCTTTCAGCAAGGAAACTAAGAGTCAAGCATTT 648
DB 550 ATTGGGCAAGCTCTCCAAATGCTTTCAGCAAGGAAACTAAGAGTCAAGCATTT 609
QY 649 ATTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGAGGCTTAACCTCAG 708
DB 610 ATTACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGAGGCTTAACCTCAG 669
QY 709 AGGACCTCAGTATGTTGTTAATTTGAG 736
DB 670 AGGACCTCAGTATGTTGTTAATTTGAG 697

RESULT 4

US-09-877-650-12

Sequence 12, Application US/09877650
Patent No. US20020169117A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)213-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: hURANKL (full length)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..951
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-877-650-12

Query Match 10.9%; Score 126; DB 9; Length 954;
Best Local Similarity 72.6%; Pred. No. 2.2e-30;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAGTATTGCTAAGATGCAATCTGACGCTCAGCCTTCAACTGATCTTTTA 524
DB 449 CATGTTAGATCTGGCCCAAGAGAGCAAGCTTGAAGCTCAGCCTTTCATCTCACTA 508
QY 525 TTAATACCATCAATATCCATGAGGCT--CATTAACGAGTCTTCTTCTGGAACATG 582
DB 509 TTAATGCGACGACATCTGCTGCTCCATTAAGTGAAGTCTGCTCTGTTACCATG 568
QY 583 ACCAAGATTGGGCAAGCTCTCCAAATGCTTTCAGCAAGGAAACTAAGAGTCA--- 639
DB 569 ATCGGGGTTGGGCCAAGATCTCCAAATGACTTTAGCAATGAAACTAATAGTTATC 628
QY 640 ---AAGCATTTATACCGGAATGCCGACATTTGCTCGACATCGGTAACCTCAGCAG 696
DB 629 AGGATGGCTTTTATACCTGTAATGCCCAACATTTGCTTTCGACATCATGAACCTCAGGAG 688
QY 697 GCCTAATCTCGAGGACCTTCAGCTA 722
DB 689 ACTTACTACAGATATCTTCAACTA 714

RESULT 5

US-09-871-856-12

Sequence 12, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA

```

? GENERAL INFORMATION:
? APPLICANT: Choi, Yongwon
? Mong, Brian
? Josien, Regis
? Steilman, Ralph
? TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
? INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
? METHODS OF USE THEREOF
?
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Klauber & Jackson
? STREET: 411 Hackensack Avenue, 4th Floor
? CITY: Hackensack
? STATE: New Jersey
? COUNTRY: USA
? ZIP: 07601
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/017,910
? FILING DATE: 14-Dec-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 09/447,035
? FILING DATE: 1999-11-22
? ATTORNEY/AGENT INFORMATION:
? NAME: Jackson Esq., David A.
? REGISTRATION NUMBER: 26,742
? REFERENCE/DOCKET NUMBER: 600-1-200
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-487-5800
? TELEFAX: 201-343-1684
? TELEX: 133521
?
? INFORMATION FOR SEQ ID NO: 1:
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1823 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEICAL: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..738
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
? US-10-017-910-1
?
? Query Match 10.6%, Score 122.8; DB 9; Length 1823;
? Best Local Similarity 71.8%; Pred. No. 3.6e-29;
? Matches 191; Conservative 0; Mismatches 67; Indels 8; Gaps 2;
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? 465 CAGGAGAGTATTCTCTAAGATGGCAATCCTGACGCTCAGCCTTCAACTGATCTTGTGA 524
? ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
? Db 233 CATGTTGATGATCGCCCAAGAGAGCAAGCTTGAGGCTCAGCCTTTCATCTCAGCTA 292
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? 525 TTAATACATCAATAATCCATGAGGCT--CATAAACGAGTCTTCTTCTTGGAAACATG 582
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? Db 293 TTAATGCCACCGACATCCCATCTGTGTTCCCATTAAGTAGAGTCTCTCTTTGGTACCATG 352
?
? 583 ACCAAGATTGGGCAAACTCTCCCAACATGACTTCACGAAAGAAACTAAGAGTCA--- 639
? ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
? Db 353 ATCGGGGCTGGGTTAGATCTCCCAACATGACTTTTACCAATGGAAACTAATAGTTAATC 412
?
? 640 ---AAGCATTTATTACCGAATCCGACATTTGCTCTGCAACATCGGCTAAGCTCAGAG 696
? ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
? Db 413 AGGATGGCTTTTATTACTGTATGCCAACATTTGCTTTGCACATCATGAATCTCAGGAG 472
?
? 697 GCCTAACTCTGCAGGACCTTCAGCTA 722

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Db 473 ACCTAGCTACAGAGTATCTTCAACTA 498

RESULT 7

US-09-877-650-10

Sequence 10, Application US/09877650

Patent No. US20020169117A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/877,650

FILING DATE: 08-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mus musculus

IMMEDIATE SOURCE:

LIBRARY: <Unknown>

CLONE: RANKL

FEATURE:

NAME/KEY: CDS

LOCATION: 3..884

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-877-650-10

Query Match 8.4% Score 97; DB 9; Length 1630;

Best Local Similarity 67.2% Pred. No. 7.3e-21;

Matches 170; Conservative 0; Mismatches 75; Indels 8; Gaps 2;

QY 477 TTGCTAGATGCAATCTGACCTGACCTTCACTCTTGTATTATTAATGATCA 536

DB 394 TGGCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453

QY 537 ATATCCATGAGG--CTCATATAAAGAGGCTTTCTTCTTGGAACATGACCAAGATTGGG 594

Db 454 GATCCATCCGCGGTTCCCATATAAGTCACTCTGCTCTTGGTACACGATGAGGCTGGG 513

QY 595 CAAAGCTCTCCACATGACTTTCAGCAAGCAAGAAACATTAAGTCA-----AAGGCAATT 648

Db 514 CCAAGATCTCTAACAATGACGTTAAGCAAGGAAACCTAAGGTTAACCAGATGCTTCT 573

QY 649 ATTACCGGATGCGGACATTTGCTCTGACATCGGCTAACCCTACAGAGGCTTAATCTGC 708

Db 574 ATTACCTGACGCAACATTTGCTTGGCATCATGAAACATCGGGAAGCGTACTACAG 633

QY 709 AGGACCTTCAGCT 721

Db 634 ACTATCTTACGCT 646

RESULT 8

US-09-871-856-10

Sequence 10, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent

Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/871,856

FILING DATE: 31-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139

FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1630 base pairs

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mus musculus

IMMEDIATE SOURCE:

LIBRARY: <Unknown>

CLONE: RANKL

FEATURE:

NAME/KEY: CDS

LOCATION: 3..884

RESULT 15
US-09-764-869-1690/c
; Sequence 1690, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ. ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ. ID NO 1690
; LENGTH: 12259
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (398)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-1690

Query Match 3.0%; Score 35.2; DB 10; Length 12259;
Best Local Similarly 51.2%; Pred. No. 2.7;
Matches 82; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

OY 882 CAGGAGTGGCTGCTGGCTGAGGAGACCAAGGTAATGCGCCCTGGGAGCGCCCGGAGAGA 941
DB 1983 CAGGCTGCAGGTGAGAAAGGAGGCTGAGGGCCGAGGAGTTGAGAGAGCCCTAGAGTG 1924
OY 942 GATGAGTTTGTAGGCAAGGATTTGATTTGATGATGAACCTGTGTGTTACAGCTGAAG 1001
DB 1923 GAACAGCACAGAGACTATGCAATTACTCTTAATTATCTTCCGTACAGAGCTGTGG 1864
OY 1002 CTGAGTTGTAACTCTGAACCAAGGAGCAAGCAAGCATGATGT 1041
DB 1863 GGTTAGCTGTGCTGTGAGTACAGGTCCAGGTTCCAGT 1824

Search completed: December 8, 2002, 19:37:48
Job time : 623.832 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

OM protein - protein search, using sw model

December 8, 2002, 18:34:08 ; Search time 44.7484 Seconds
(without alignments)
313.111 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAHTSLSSWKHDQDWNV....

Scoring table: BLOSUM62

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Maximum DB seq length: 200000000000

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : SPTREMBL_21:*

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1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	69	18.5	214	13	Q9DD25	Q9DD25 brachydanis
2	69	18.5	1130	15	Q88282	Q88282 snakehead
3	68	18.2	187	10	Q9FGA8	Q9FGA8 arbidopsi
4	67	18.0	296	16	Q9X2G7	Q9X2G7 thermotoga
5	67	18.0	307	10	Q9FT49	Q9FT49 arbidopsi
6	67	18.0	478	15	Q71146	Q71146 human
7	64.5	17.3	276	16	Q9J710	Q9J710 human
8	64.5	17.3	1000	4	Q9J710	Q9J710 clostridium
9	64.5	17.3	1018	4	Q6K350	Q6K350 homo sapien
10	64.5	17.3	1090	4	Q9HC88	Q9HC88 homo sapien
11	64.5	17.3	1214	4	Q9Y6M7	Q9Y6M7 homo sapien
12	63.5	17.0	297	5	Q9VCJ9	Q9VCJ9 drosophila
13	63.5	17.0	297	5	Q9VCJ9	Q9VCJ9 drosophila
14	63.5	17.0	813	16	Q9I3X9	Q9I3X9 pseudomonas
15	62.5	16.8	287	13	Q9QWY9	Q9QWY9 gallus galli
16	62	16.6	251	10	Q942B1	Q942B1 oryza sativ
			166	17	Q96ZT5	Q96ZT5 sulfolobus

17	61	16.4	322	5	Q95XD5
18	61	16.4	1530	5	Q95YV1
19	61	16.4	1101	5	Q45818
20	61	16.4	1630	16	Q8RHN7
21	60	16.1	274	15	Q8YZ14
22	60	16.1	354	15	Q8UDK4
23	60	16.1	609	15	Q8E9R7
24	60	16.1	2353	16	Q8YTT4
25	59.5	16.0	156	17	Q97516
26	59.5	16.0	216	16	Q8XK87
27	59.5	16.0	216	16	Q8XD17
28	59.5	16.0	261	16	Q92NKK
29	59.5	16.0	427	16	Q9K9G9
30	59	15.8	157	16	Q68768
31	59	15.8	364	16	Q8RFE0
32	58.5	15.7	91	5	Q22506
33	58.5	15.7	237	2	Q9X6N2
34	58.5	15.7	316	4	Q96BW9
35	58.5	15.7	1171	17	Q97BJ7
36	58	15.5	308	16	Q8R5Y5
37	58	15.5	330	17	Q58765
38	58	15.5	646	10	Q81015
39	57.5	15.4	262	2	Q9PAC1
40	57.5	15.4	391	2	Q9JRL2
41	57.5	15.4	425	16	Q99YB2
42	57.5	15.4	729	16	Q92IP3
43	57.5	15.4	830	11	Q99LPE
44	57.5	15.4	1514	5	Q9NMR3
45	57.5	15.4	1514	5	Q9VUD0
					Q95XD5 caenorhabditis
					Q95YV1 drosophila
					Q45818 caenorhabditis
					Q8RHN7 fusobacter
					Q8YZ14 anaerobac
					Q8UDK4 agrobacter
					Q8E9R7 rhizobium
					Q8YTT4 ralsstonia
					Q97516 sulfolobus
					Q8XK87 salmonella
					Q8XD17 escherichia
					Q92NKK rhizodium
					Q9K9G9 bacillus h
					Q68768 yersinia p
					Q8RFE0 fusobacter
					Q22506 caenorhabditis
					Q9X6N2 streptomyces
					Q96BW9 homo sapien
					Q97BJ7 thermoplasma
					Q8R5Y5 fusobacter
					Q58765 pyrococcus
					Q81015 arabidopsis
					Q99YB2 streptococcus
					Q92IP3 streptococcus
					Q99LPE rickettsia
					Q9NMR3 mus muscula
					Q9VUD0 drosophila

ALIGNMENTS

	RESULT 1				
ID	Q9DDZ5	PRELIMINARY;	PRT;	214 AA.	
AC	Q9DDZ5				
DT	01-MAR-2001 (TREMBLrel_16, Created)				
DT	01-MAR-2001 (TREMBLrel_16, Last sequence update)				
DE	01-MAR-2002 (TREMBRel_20, last annotation update)				
GN	TNFSF10L-like protein.				
OS	Brachydanio rerio (zebrafish) (zebra danio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. NCBI_TaxID=7955; [1]__SEQUENCE FROM N.A. RA Bobe J., Goetz F.W.; RT "Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary." RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001). DR EMBL AF250041. AAG47640.1; - DR HSSP; P50591; IDOG. DR ZFIN; ZDB-GENE-010801-1; tnfsf10l. DR InterPro: IPR003636; TNF_abC. DR InterPro: IPR000478; TNF_family. DR Pfam; PF00229; TNF; 1. DR ProDom; PD002012; TNF_abC; 1. DR SMART; SMO0207; TNF; 1. DR PROSITE; PS50049; TNF_2; 1. SQ SEQUENCE 214 AA; 24093 MW; 98C00247AFF691AA CRC64;				
Query Match		18.5%;	Score 69;	DB 13;	Length 214;
Best Local Similarity		31.2%;	Fred. NO. 1.2;		
Matches 15;	Conservative 13;	Mismatches 18;	Indels 2;	Gaps 1;	
OY	1 HEAHTSLSWKHODMANVSNNFTSNCKLRV--KGIYYRNADICSRH 46	:	: :	:	:
Db	76 HQSCHRPHTWANKSGFAHLTYMTLTNGRLRVPDQGRIYLVSQVFERY 123	:	:	:	:

RESULT 2
088282 PRELIMINARY: PRT: 1130 AA.
AC 088282:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope protein.
GN ENV.
OS Snakehead retrovirus.
OC Viruses: Retroviridae; Retroviridae; Epsilonretrovirus.
NCBI_TaxID=40270;
RX MEDLINE=96211493; PubMed=8648695;
RA Hart D., Fierichs G.N., Rambaut A., Onions D.E.;
RT "Complete nucleotide sequence and transcriptional analysis of
snakehead fish retrovirus."
RL J. Virol. 70:3606-3616(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Hart D., Fierichs G.N., Rambaut A., Ronalds R.J., Onions D.E.;
RT "Evidence for a new retrovirus genus of piscine origin."
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U26458; AAC54858.1; -
SQ SEQUENCE 1130 AA; 128317 MW; B6A4F8095E4F0D3F CRC64;
Query Match 18.5%; Score 69; DB 15; Length 1130;
Best Local Similarity 25.9%; Pred. No. 8.7; Indels 30; Gaps 4;
Matches 22; Conservative 11; Mismatches 22;
OY 6 TSLSWKKHD-----OWANVSNMTFSGNKLRYKGIYRNADICSRHRV-----TSA 51
DB 476 SSGNSWKAIEDIKRKQK----QKCYFSGKLRKIGTDYEEDTCKPLIGLGFIPITGV 531
OY 52 GLTLQ-----DLQWCM 64
DB 532 TKTLKGTWTTAVVKIDLDQWVDI 556
RESULT 3
09FGA8 PRELIMINARY: PRT: 187 AA.
ID 09FGA8:
AC 09FGA8:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Similarity to pollen-specific protein Bnml.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB026650; BAB10289.1; -
SQ SEQUENCE 187 AA; 20056 MW; 305781D3A0738AEA CRC64;
Query Match 18.2%; Score 68; DB 10; Length 187;
Best Local Similarity 32.8%; Pred. No. 1.3; Indels 10; Gaps 2;
Matches 22; Conservative 9; Mismatches 26;
OY 1 HEAH-----KTSLSWKKHDOWANVSNMTFSGNKLRYKGIYRNADICSRHRVTSAGL 53
DB 102 HDHYVGIILSLKSLLELDKSPFANYDVAVSGDDTRRVAGLVEKNKNTDASK---TLMEM 158
OY 54 TLQDLQ 60

DB 159 TLQMDL 165
RESULT 4
09X2G7 PRELIMINARY: PRT: 296 AA.
ID 09X2G7:
AC 09X2G7:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein TM1852.
GN TM1852.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Garrett M.M.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 391:323-329(1999).
DR EMBL: AE001822; AAC36914.1; -
DR TIGR: TM1852; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 296 AA; 34197 MW; 11B3960CA5C3D2C6 CRC64;
Query Match 18.0%; Score 67; DB 16; Length 296;
Best Local Similarity 27.3%; Pred. No. 3.1; Indels 19; Gaps 3;
Matches 15; Conservative 11; Mismatches 19;
OY 14 DQDW---ANVSNMTFSGNKLRYKGIYRNADICSRHRVTSAGLTLQDLQW 62
DB 244 EEDWKEFGGVNPNVSDAMIEYGYVYGADNC---IALATIPVEKWKWC 294
RESULT 5
09FT49 PRELIMINARY: PRT: 307 AA.
ID 09FT49:
AC 09FT49:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Hypothetical 34.9 kDa protein.
GN T25B15_100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL132972; CAC07924.1; -
KW Hypothetical protein.
SQ SEQUENCE 307 AA; 34863 MW; DC8746CB47D8F92E CRC64;
Query Match 18.0%; Score 67; DB 10; Length 307;
Best Local Similarity 18.3%; Pred. No. 3.3; Indels 22; Gaps 2;
Matches 15; Conservative 19; Mismatches 26;


```

OY 1 HEAKTSLSSMKHDDM-----ANVSNMFTSNGKLRKGYRN 39
DB 149 HDEKYLSTFWIRNKEMKVRSEHHVLYGARTSMKKTCQHHLHPYSOG-ITINGVLYTG 207
OY 40 ADICSRHRVTSAGLTLODLQW 61
DB 208 AWDDKCVLMSFDLTSBDCVGM 229

RESULT 6
OY 071146 PRELIMINARY: PRT: 478 AA.
ID 071146
AC 071146
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein gp120 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V22
RC MEDLINE=96039896; PubMed=7576917;
RA Quinones-Mateu M.E., Dopazo J., Este J.A., Rota T.R., Domingo E.;
RT "Molecular characterization of human immunodeficiency virus type 1
RT isolates from Venezuela."
RL AIDS Res. Hum. Retroviruses 11:605-616(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VE2;
RC MEDLINE=97000986; PubMed=8844016;
RA Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
RT "Point mutant frequencies in the pol gene of human immunodeficiency
RT virus type 1 are two- to threefold lower than those of env."
RL AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
DR Interpro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
FT NON_TER 1 478
FT SEQUENCE 478 AA; 53554 MW; 103F636765B51D92 CRC64;
SO Query Match 18.0%; Score 67; DB 15; Length 478;
Best Local Similarity 25.0%; Pred. No. 5.5; 27; Indels 24; Gaps 3;
Matches 21; Conservative 12; Mismatches 127

OY 2 EAHKTSLSMKHDDM-----DMANVSNMFTSNGKLRKGYRNADIC 43
DB 74 QMHEDITSLW--DOSLRKCVKLPFLCYLTDCTDGMNATNTNISGGAMERG---EIKNC 127
OY 44 SRHRVTSAGLTLODLQWLCNLRIT 67
DB 128 SFNITTSGEKMKKEALFYNDIV 151

RESULT 7
OY 097130 PRELIMINARY: PRT: 276 AA.
ID 097130
AC 097130
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Possible glucanotransferase (putative endo alpha-1,4
DE polygalactosaminidase related protein).
GN CA00736.
OS Clostridium acetobutylicum.
OS Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OS Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_Taxid=1488;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RC MEDLINE=21359325; PubMed=1146286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Hiti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007588; AAK78712.1; -
DR Transferase; Complete proteome.
SO SEQUENCE 276 AA; 32104 MW; 2EFC06A77E4791B CRC64;

OY 10 SKRHDQDQVANSNMFTSN-----GK-LRVKGI---YRNADICSRHRVTSAGLTLODL 58
DB 105 NWK-DESMIDVSNLKMNDYVNTLGNLKNKGVDGFDDNDYKSKYKDKSMFGLINI 162

RESULT 8
OY 0901B9 PRELIMINARY: PRT: 1000 AA.
ID 0901B9
AC 0901B9
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bicarbonate transporter.
GN BT.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Komer M.F.;
RA "Cloning of a HCO3 transporter, NT2-NBC, from human brain, similar to
RT both the Anion exchangers (AEs) and the Na/Bicarbonate Cotransporters
RT (NBCs).";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF053755; AAF21720.1; -.
DR HSSP: P02730; IBNX.
DR Interpro: IPR001717; Anion_exchange.
DR Pfam: PF00955; HCO3_cotransp. 1.
DR PRINTS: PR01231; HCO3TRANSPORT.
DR TIGRPFAM: TIGR00834; ae; 1.
SO SEQUENCE 1000 AA; 112501 MW; 93FAA40A3141F8F7 CRC64;

OY 7 SLSMKRHDQDQVANSNMFTSNGKLRKGYRNADICSRHRVTSAGLTLODLQW 62
DB 564 TLAQMKNDITANISWNLTVSECK-KLRGVFLSA--CGHR-----GPIYPOVLRWC 614

RESULT 9
OY 060350 PRELIMINARY: PRT: 1018 AA.
ID 060350
AC 060350
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium bicarbonate cotransporter2.
GN SBC2.
OS Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=RETINA;

RA Ishibashi K., Sasaki S., Marumo F.;

RT "Molecular cloning of a new sodium bicarbonate cotransporter cDNA from

RL human retina.";

DR Biochem. Biophys. Res. Commun. 0:0-0(1998).

DR EMBL; AB012130; BAA25898.1; -.

DR HSSP; P02730; IBNX.

DR InterPro; IPR001717; Anion_exchange.

DR InterPro; IPR003020; HCO3_cotransp.

DR Pfam; PF00955; HCO3_cotransp. 1.

DR PRINTS; PR01231; HCO3TRNSPORT.

DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1018 AA; 114204 MW; A37799D93AE30BC CRC64;

Query Match 17.3%; Score 64.5; DB 4; Length 1018;

Best Local Similarity 32.2%; Pred. No. 28;

Matches 19; Conservative 12; Mismatches 17; Indels 11; Gaps 5;

QY 7 SLSWKHDQMA-NVS--NMTFSGKLRVKGIIYRNADICSRHRYTSAGLTLDQLWC 62

DB 564 TLAQKKKNITAHNISMWNLTVSECK-KLRGVFLGSA--CGHH-----GPIIDVLEWFC 614

RESULT 10

09HC88 PRELIMINARY; PRT; 1090 AA.

AC 09HC88; PRT; 1090 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE Sodium bicarbonate cotransporter 2b.

GN NDC2B.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RA Pushkin A., Abuladze N., Newman D., Hwang J., Kurtz I.;

RT "Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete

RL cds.";

DR EMBL; AF089726; AAG16773.1; -.

DR HSSP; P02730; IBNX.

DR InterPro; IPR001717; Anion_exchange.

DR InterPro; IPR003020; HCO3_cotransp.

DR Pfam; PF00955; HCO3_cotransp. 1.

DR PRINTS; PR01231; HCO3TRNSPORT.

DR TIGRFAMs; TIGR00834; ae; 1.

GN

OS SLCA47.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SKETRAL; MUSCLE;

RA MEDLINE=9278433; PubMed=10347222;

RA Pushkin A., Abuladze N., Lee I., Newman D., Hwang J., Kurtz I.;

RT "Cloning, tissue distribution, genomic organization, and functional

RT characterization of NDC3, a new member of the sodium bicarbonate

RL J. Biol. Chem. 274:16569-16575(1999).

DR EMBL; AF047033; AAD38322.1; -.

DR HSSP; P02730; IBNX.

DR InterPro; IPR001717; Anion_exchange.

DR InterPro; IPR003020; HCO3_cotransp.

DR Pfam; PF00955; HCO3_cotransp. 1.

DR PRINTS; PR01231; HCO3TRNSPORT.

DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1214 AA; 136042 MW; EF20350B5BF5267 CRC64;

Query Match 17.3%; Score 64.5; DB 4; Length 1214;

Best Local Similarity 32.2%; Pred. No. 35;

Matches 19; Conservative 12; Mismatches 17; Indels 11; Gaps 5;

QY 7 SLSWKHDQMA-NVS--NMTFSGKLRVKGIIYRNADICSRHRYTSAGLTLDQLWC 62

DB 778 TLAQKKKNITAHNISMWNLTVSECK-KLRGVFLGSA--CGHH-----GPIIDVLEWFC 828

RESULT 12

09VCJ9 PRELIMINARY; PRT; 297 AA.

AC 09VCJ9; PRT; 297 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE CG16710 protein.

GN CG16710.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Ephydroidea; Diptera; Brachycera; Muscomorpha;

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amandas P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

```

Query Match      17.0%; Score 63.5; DB 16; Length 813;
Best Local Similarity   28.8%; Pred.No. 29;
Matches    19; Conservative    11; Mismatches    23; Indels    13; Gaps    3

QY       6 TSLSSKHHQDDANVANSNMFTSNCK-LRVVGI-----YYRNADICSRHRYT---SAG 52
Db       711 TAYLGKKRPDANNNRIGALFFDSKYRLDGVESFGRRQYSTTYTVDVLSQIRLTPDDQLS 770
        | :|:||||| ||::|::| | | :|:|:|:| |
QY       53 LFLDL 58
Db       771 LGIGNL 776
        | :|:|

RESULT 14
O90WT9          PRELIMINARY; PRT; 287 AA.
AC O90WT9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DT TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
RT ovary." ;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AL23702.1; .
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR Prodom; PD002012; TNF_abc; 1.
DR PROSITE; PS50049; TNF_2; 1.
SO SEQUENCE 287 AA; 32092 MW; D806E1C95087B108 CRC64;

Query Match      16.9%; Score 63; DB 13; Length 287;
Best Local Similarity   28.6%; Pred.No. 9.5;
Matches    16; Conservative    14; Mismatches    24; Indels    2; Gaps    1;

QY       7 SLSSSKHQDDANVANSNMTFSNGKLFRK--GIYYRNADICSRHRYTSAGITLDQL 60
Db       156 ALTREWEDSTLIHSQNITYRGRLRNVQAGKYYVSQLYFRYSRDGAGRARSVPGL 211
        ::|:|::|:|:|:|:|:| ||::| | | | | | | | | |
        | :|:|:|:|:|:|:| ||::| | | | | | | | | |

RESULT 15
O94ZB1          PRELIMINARY; PRT; 251 AA.
ID O94ZB1;
AC O94ZB1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE B106OH01.30 protein (OSUJB0021A09.1 protein).
GN B106OH01.30 OR OSUJB0021A09.1.
OS Oryza sativa (Rice), and
OS Oryza sativa (Japanese cultivated group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530; 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NIPPONbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:B106OH01." ;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 8, 2002, 17:28:38 ; Search time 12.7226 Seconds

(without alignments)
221.684 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Sequence: 1 HEAHTKTSLSMKHDDMANV.....TSAGLTLDIQLMCNLRH 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	47.7	317	1	TN11_HUMAN
2	175	46.9	318	1	TN11_RAT
3	172	46.1	316	1	TN11_MOUSE
4	63.5	17.0	263	1	PYRF_PICAN
5	61.5	16.5	501	1	CSD2_DROME
6	59.5	16.0	216	1	SGAH_ECOLI
7	59.5	16.0	329	1	IPNS_MOUSE
8	58.5	15.7	251	1	Y108_CHLTR
9	58.5	15.7	269	1	IL1B_TRIUV
10	58	15.5	119	1	YRAN_HAELN
11	57.5	15.4	478	1	DISR_AGRH
12	57.5	15.4	677	1	RN14_YEAST
13	57.5	15.4	2156	1	FCG1_MOUSE
14	56.5	15.1	404	1	FCG1_MOUSE
15	56	15.0	196	1	TRAP_ECOLI
16	56	15.0	484	1	SLT2_YEAST
17	56	15.0	785	1	APR2_YEAST
18	55.5	14.9	144	1	IAAE_HORVU
19	55.5	14.9	680	1	KALM_HUMAN
20	55.5	14.9	837	1	TP11_HUMAN
21	55	14.7	500	1	CP11_RABIT
22	54.5	14.6	310	1	SC65_YARLI
23	54.5	14.6	333	1	IPNS_STRLP
24	54.5	14.6	855	1	ENV_HV1A2
25	54.5	14.6	1451	1	TPN5_YEAST
26	54	14.5	261	1	TPN5_AOTTR
27	54	14.5	261	1	TPN5_CALTA
28	54	14.5	261	1	TPN5_HUMAN
29	54	14.5	261	1	TPN5_MACMU
30	54	14.5	318	1	ATPS_YEAST
31	54	14.5	851	1	NDU1_YEAST
32	54	14.5	886	1	ORC1_KLUDU
33	53.5	14.3	329	1	IPNS_STRLP

34	53.5	14.3	2255	1	RRPL_SVS	Q08434	sinlan viru
35	53	14.2	220	1	PIS_YEAST	P06197	saccharomyc
36	53	14.2	334	1	GUB_CLOTH	P29716	clostridium
37	53	14.2	377	1	PROB_MEIRU	O92598	meiosternus
38	53	14.2	453	1	PPAL_SCHPO	P08091	schizosacch
39	53	14.2	475	1	PRTG_ERWCH	O07162	erwinia chr
40	53	14.2	636	1	SGA7_HUMAN	O09884	homo sapien
41	53	14.2	764	1	PAG_BACAN	P13423	bacillus an
42	53	14.2	869	1	POZ1_SCICO	P20043	sciara copr
43	53	14.2	1006	1	BCAL_IACBE	O13683	schizosacch
44	53	14.2	1237	1	VDY2_SCHPO		
45	53	14.2	1242	1	MSH6_YEAST	Q03834	saccharomyc

ALIGNMENTS

RESULT 1
ID TN11_HUMAN STANDARD: PRT; 317 AA.
AC O14788: 014723; Q9P203; Q96Q17;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast
DE differentiation factor) (ODF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP TISSUE=bone marrow, and peripheral blood;
RC MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [2]
RP TISSUE=Lymph node;
RC MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RP TISSUE=Thymocytes;
RC MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Aron J., Robinson E., Orlicki J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [5]
RP TISSUE=Tongue;
RC TISSUE=Tongue;

Query Match	47.7%	Score 178	DB 1	Length 317
XX MEDLINE=20175237; PubMed=10708588;				
RA Nagai M., Kyakumoto S., Sato N.;				
RT "Cancer cells responsible for humoral hypercalcemia express mRNA				
RT encoding a secreted form of ODF/TRANCE that induces osteoclast				
RT formation.";				
RL Biochem. Biophys. Res. Commun. 269:532-536(2000).				
CC -I- FUNCTION: Cytokine that binds to TNFRSF11b/Obp and to				
CC TNFRSF11a/RAK. Osteoclast differentiation and activation factor.				
CC Augments the ability of dendritic cells to stimulate naive T-cell				
CC proliferation. May be an important regulator of interactions				
CC between T cells and dendritic cells and may play a role in the				
CC regulation of the T cell-dependent immune response. May also play				
CC an important role in enhanced bone-resorption in humoral				
CC hypercalcemia of malignancy.				
CC -I- SUBUNIT: Homotrimer (By similarity).				
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);				
CC Secreted (isoform 2). A soluble form of isoform 1 arises by				
CC proteolytic processing (By similarity).				
CC -I- ALTERNATIVE PRODUCTS: 3 isoforms: 1 (shown here), 2/SODF and 3;				
CC are produced by alternative splicing.				
CC -I- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT				
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,				
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.				
CC -I- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.				
CC -I- PTM: The soluble form of isoform 1 derives from the membrane form				
CC by proteolytic processing (By similarity). The cleavage may be				
CC catalyzed by ADAM17.				
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.				
CC -----				
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CC or send an email to license@sdb.ch).				
CC -----				
DR EMBL: AF019047; AAB86811.1; -				
DR EMBL: AF053712; AAC39731.1; -				
DR EMBL: AB064269; BAB79694.1; -				
DR EMBL: AB061227; BAB71768.1; -				
DR EMBL: AB064270; BAB79695.1; -				
DR EMBL: AF013171; AAC51762.1; -				
DR EMBL: AB037599; BAA90488.1; -				
DR HSSP: P50591.1; D0G				
DR Genew: H0NC.1; I926; TNFSF11.				
DR MIM: 602642; -				
DR InterPro: IPR003636; TNF_abc.				
DR InterPro: IPR000478; TNF_family.				
DR Pfam: PF00229; TNF; 1.				
DR Prodom: PD002012; TNF_abc; 1.				
DR SMART: SM00207; TNF; 1.				
DR PROSITE: PS00251; TNF_1; FALSE_NEG.				
DR PROSITE: PSS0049; TNF_2; 1.				
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;				
KW Signal-anchor; Alternative splicing.				
FT CHAIN 1 317				
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY				
FT MEMBER 11, MEMBRANE FORM.				
FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY				
FT MEMBER 11, SOLUBLE FORM (BY SIMILARITY).				
FT CYTOPLASMIC (POTENTIAL).				
FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)				
FT (POTENTIAL).				
FT EXTRACELLULAR (POTENTIAL).				
FT CLEAVAGE (BY SIMILARITY).				
FT N-LINKED (GLCNAC. .) (POTENTIAL).				
FT N-LINKED (GLCNAC. .) (POTENTIAL).				
FT MISSING (IN ISOFORM 3).				
FT MISSING (IN ISOFORM 2).				
FT A -> G (IN REF. 4).				
FT CONFLICT 194 194				
FT SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;				

```

Best Local Similarity 60.0%; Pred.No. 7,8e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY      3 AHKSLSSSKHDDDMANVSNMTFSNGKLRPK--GIYYRNADICSRHRVTSAGLTLDLQ 60
Db       179 SHKYSLSWYHDRCGMARISNMFTSNGKLIVNODGFYLLANICFRHHETSGDLATYEQL 238
          :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 2
ID      TN1L_RAT STANDARD: PRT; 318 AA.
TN1L_RAT
AC QSESSE2: Q91Z19;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast
DE differentiation factor) (ODF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Rattus norvegicus (Rat).
OC Eumariota: Metazoa: Chordata: Cranialta; Euteleostomi;
OC Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Tibial bone;
RX MEDLINE=20540945; PubMed=11092396;
RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL [2].
RN SEQUENCE OF 266-318 FROM N.A.
RP STRAIN=Fischer 344;
RX PubMed=11804028;
RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savvas A.,
RA Saidel F.F., Popoff S.N., Lengner C., van Hul W., Choi Y.,
RA Marks S.C. Jr.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the TNFSF11 (TRANCE, RANKL, ODF, OpGn) gene.";
RL Int. J. Dev. Biol. 45:853-859(2001).
CC -I- FUNCTION: Cytokine that binds to TNFRSF11B/OpG and to
CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
CC Augments the ability of dendritic cells to stimulate naive T-cell
CC proliferation. May be an important regulator of interactions
CC between T cells and dendritic cells and may play a role in the
CC regulation of the T cell-dependent immune response. May also play
CC an important role in enhanced bone-resorption in humoral
CC hypercalcaemia of malignancy.
CC -I- SUBUNIT: Homotrimer (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -I- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
CC -I- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF187319; AAG17031.1; -.
CC EMBL: AF245669; AAL23963.1; -.
CC HSSP: P50591; IDOG.
CC InterPro: IPR003636; TNF_abC.
CC Interpro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF_1.
CC

```


CC TRABECULAR BONE AND LUNG.
 CC -1- PTH: N-glycosylated
 CC -1- PTH: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -1- DISEASE: DEFICIENCY IN TNFSF1 RESULTS IN FAILURE TO FORM LOBULO-
 CC OP MEMBRANS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS WITH
 CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
 CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
 CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
 CC HYPERTROPHIC CHONDROCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC
 CC EMBL: AF013170; AAC1061.1;
 CC EMBL: AF019048; AAB6681.1;
 CC EMBL: AF053713; AAC4011.1;
 CC EMBL: AB008426; BAA25425.1;
 CC EMBL: AB022039; BAA36970.1;
 CC EMBL: AB022036; BAA36970.1; JOINED.
 CC EMBL: AB022037; BAA36970.1; JOINED.
 CC EMBL: AB022038; BAA36970.1; JOINED.
 CC EMBL: AB032771; BAA97257.1;
 CC EMBL: AB032772; BAA97257.1;
 CC EMBL: AB036798; BAA97259.1;
 CC PDB: 1J7Z; 13-SEP-01.
 CC PDB: 1J7Z; 13-MAR-02.
 CC PDB: 1J7Z; 13-SEP-01.
 CC MGI: 1100089; Tnfsl.
 CC InterPro: IPR0003636; TNF_family.
 CC Pfam: PF00229; TNF; 1.
 CC SMART: SMO0207; TNF; 1.
 CC PROSITE: PS00251; TNF_1; FALSE_NEG.
 CC PROSITE: PS50049; TNF_2; 1.
 CC Cytokine: Differentiation; Receptor; Glycoprotein; Transmembrane;
 CC Signal-anchor: 3D-structure; 316
 CC CHAIN 1 316
 CC FT CHAIN 139 316
 CC FT DOMAIN 1 48
 CC FT TRANSMEM 49 69
 CC FT
 CC FT DOMAIN 70 316
 CC FT SITE 138 316
 CC FT CARBOHYD 197 197
 CC FT CARBOHYD 262 262
 CC FT VARSPLIC 1 117
 CC FT VARSPLIC 1 44
 CC FT
 CC FT CONFLICT 99 99
 CC FT CONFLICT 141 143
 CC FT SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;
 CC
 CC Query Match 46.18; Score 172; DB 1; Length 316;
 CC Best Local Similarity 56.7%; Pred. No. 4.4e-14;
 CC Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;
 CC
 CC 3 AKHTSSWKKHODMANVSMFNSGKLVK--GIYYNADICSHRYTSAGLTLQDL 60
 CC Db 178 SHKVTLSWYHDGMAKISNMLTSGKLVKLVNODGFYUANYICFHHHTSSGVPIDYDL 237
 CC RESULT 4

PYRE_PICAN
 ID PYRE_PICAN STANDARD: PRT; 263 AA.
 AC Q06375;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
 DE (OMPDecase) (OMPDecase) (Uridine 5'-monophosphate synthase) (UMP
 DE URS3).
 OS Pichia angusta (Yeast) (Hansenula polymorpha).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetaceae; Saccharomycetaceae; Pichia.
 RN [1] TaxID=4905;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94128354; PubMed=7764392;
 RT "Cloning and sequencing of the ura3 locus of the methylophilic yeast
 RT Hansenula polymorpha and its use for the generation of a deletion by
 RT gene replacement."
 RL Appl. Microbiol. Biotechnol. 40:361-364(1993).
 CC -1- CATALYTIC ACTIVITY: Orotidine 5'-phosphate -> UMP + CO(2).
 CC -1- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
 CC -1- SIMILARITY: BELONGS TO THE OMP DECARBOXYLASE FAMILY.
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 CC
 CC EMBL: X69461; CAA49221.1;
 CC PIR: S31323; S31323.
 CC DR HSSP: P03962; IDGW.
 CC InterPro: IPR001754; OMPDecase.
 CC Pfam: PF00215; OMPDecase; 1.
 CC PROSITE: PS00156; OMPDecase; 1.
 CC Pyrimidine biosynthesis; Lyase; Decarboxylase.
 CC ACT_SITE 92
 CC FT SEQUENCE 263 AA; 29275 MW; 0934EF673B03A820 CRC64;
 CC
 CC Query Match 17.0%; Score 63.5; DB 1; Length 263;
 CC Best Local Similarity 39.5%; Pred. No. 1.2;
 CC Matches 17; Conservative 7; Mismatches 12; Indels 7; Gaps 2;
 CC
 CC 14 DQWNAVNSMTFNSGKLVKGIYYR--ADICSHRYTSAGL 53
 CC Db 90 DRKFADIGNTV---KLYKGGIYRTSKWADITNAHGYTGAGI 128
 CC RESULT 5
 CC CS2D_DROME
 AC CS2D_DROME STANDARD: PRT; 501 AA.
 ID CS2D_DROME
 AC 09VMT6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Probable cytochrome P450 2B42 (EC 1.14.14.1) (CYP2B4).
 GN CYP2B4 OR CG6081.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D.; Celinkner S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
 RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Tandell M.D., Zhang Q., Chen L.X.,
 RA Branton D.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,
 RA Jallat M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Kimmel B.E., Kodira C.D., Kraft A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein J., Wu D., Yang S., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195(2000).
 RL [2]
 RN CONCEPTUAL TRANSLATION.
 RP Nelson B.;
 RA Unpublished observations (SEP-2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND
 CC IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
 CC (potential).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
 CC gene model prediction.

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CC EMBL: AE003609; AAF52225.1; ALT_SPG.
 DR FlyBase: FBgn0031688; CYP28A2.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 DR Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
 KM Endoplasmic reticulum; Hypothetical similarity.
 FT BINDING 446 446 HEME (BY SIMILARITY).
 SO SEQUENCE 501 AA; 36222 MW; 9AD85F249390A655 CRC64;

Query Match 16.5%; Score 61.5; DB 1; Length 501;
 Best Local Similarity 20.8%; Pred. No. 4.6;
 Matches 21; Conservative 11; Mismatches 34; Indels 35; Gaps 4;

OY 1 HEAHTISLSSKHHODMANVSN-----MTFSNGKL-----RVKCI 35
 DB 93 HKIYATDRSP--HNEMENIVYKKTDMILGNPVLGDGEMKRSRIMPALSPNRYKAV 151
 OY 36 YYRNADICSR-----HRYTSAGLTLDLOLMCNIRII 67
 DB 152 YEVSOVCCKKFEYIRPOQOMATSEGLDAMDLSICYTEEV 192

RESULT 6
 SCGH_ECOLI STANDARD; PRT; 216 AA.
 AC P39304;
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Probable hexulose 6-phosphate synthase (EC 4.1.2.-) (HUMPS) (D-arabino
 DE 3-hexulose 6-phosphate formaldehyde lyase).
 OS SCGH OR B4196.
 OC Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RX MEDLINE=9534362; PubMed=7610040;
 RX MEDLINE=9534362; PubMed=7610040;
 RX Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 RA Blattner F.R.;
 RT "Analysis of the *Escherichia coli* genome VI: DNA sequence of the
 RT region from 92.8 through 100 minutes";
 RT Nucleic Acids Res. 23:2105-2119(1995).
 RN [2]
 RP DISCUSSION OF SEQUENCE.
 RA Reizer J., Charbit A., Reizer A., Sailer M.H. Jr.;
 RT "Novel phosphotransferases system genes revealed by bacterial genome
 RT analysis: operons encoding homologues of sugar-specific permease
 RT domains of the phosphotransferase system and pentose catabolic
 RT enzymes";
 RT Genome Sci. Technol. 1:53-75(1996).
 RN [3]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=97419490; PubMed=9274005;
 RA Reizer J., Reizer A., Sailer M.H. Jr.;
 RT "Is the ribulose monophosphate pathway widely distributed in
 RT bacteria?";
 RT Microbiology 143:2519-2520(1997).
 CC -1- FUNCTION: CONDENSATION OF D-RIBULOSE 5-PHOSPHATE WITH FORMALDEHYDE
 CC TO FORM D-ARABINO-6-HEXULOSE 3-PHOSPHATE.
 CC -1- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
 CC SCGH AND SGAE.

CC -1- SIMILARITY: BELONGS TO THE HUMPS FAMILY.
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CC EMBL: U14003; AAA97092.1;
 DR EMBL: AE000491; AAC77153.1;
 DR SWISS-2DPAGE: P39304; COLI.
 DR Ecocore: EG12496; sgah.
 DR InterPro: IPR001754; OMPdecase.
 DR Pfam: PF00215; OMPdecase; 1.
 KM Lyase; Complete permease.
 SO SEQUENCE 216 AA; 23578 MW; EC8490DA1D02D824 CRC64;

Query Match 16.0%; Score 59.5; DB 1; Length 216;
 Best Local Similarity 23.6%; Pred. No. 3.1;
 Matches 17; Conservative 16; Mismatches 28; Indels 11; Gaps 3;

QY 6 TSLSWKHDQW--ANVSNMFTSNGK-LVKKGIYRRNADICSRHRT-----SAGLT 54
 ID 114 TGVWTEQAOQNRADICGIVYHRSRDAQAGVANGVADITAIKRLSDMGKVTYTGGLA 173
 Db 55 LODDOLWCLMRTI 66
 174 LEDLPLFKGIP 185

RESULT 7
 ID IPNS_STRCL STANDARD: PRT: 329 AA.
 AC P10621;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Isopenicillin N synthetase (EC 1.-.-.-) (IPNS) (Isopenicillin N synthase).
 GN PCBC.
 OS Streptomyces clavuligerus.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OX Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
 RA MEDLINE=88212175; PubMed=3130293;
 RA Leskijä B.K., Aharonowitz Y., Meyerech M., Wolfe S., Vining L.C.,
 RT Westlake D.W.S., Jensen S.E.;
 RT "Cloning and nucleotide sequence determination of the isopenicillin N
 RL synthetase gene from Streptomyces clavuligerus.";
 CC Gene 62:187-196 (1988).
 CC -1- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS
 CC FROM DELTA-L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE (ACV) TO
 CC FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
 CC -1- CATALYST: IRON AND ASCORBATE.
 CC -1- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND
 CC CEPHALOSPORIN.
 CC -1- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
 CC OXIDOREDUCTASES
 CC -----
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 CC -----
 CC EMBL: M19421; AAA26770.1; -;
 CC EMBL: A01132; CA00131.1; -;
 CC DR PIR: A29894; A29894.
 CC DR HSSP: P05326; 1BLZ.
 CC DR InterPro: IPR005123; 2PG-fell_Oxy.
 CC DR InterPro: IPR002283; IPNS_synth.
 CC DR InterPro: IPR002057; Isopen_N_synth.
 CC Pfam: PF03171; 2OG-fell_Oxy; 1.
 CC PRINTS: PR00682; IPNSYNTHASE.
 CC DR PROSITE: PS00185; IPNS_1; 1.
 CC DR PROSITE: PS00186; IPNS_2; 1.
 CC KW Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C.
 CC FT METAL 212 212 IRON (BY SIMILARITY).
 CC FT METAL 214 214 IRON (BY SIMILARITY).
 CC FT METAL 268 268 IRON (BY SIMILARITY).
 CC SQ SEQUENCE 329 AA; 36958 MW; 71AA1CCE9514761C CRC64;

Query Match 16.0%; Score 59.5; DB 1; Length 329;
 Best Local Similarity 25.7%; Pred. No. 5;
 Matches 18; Conservative 10; Mismatches 33; Indels 9; Gaps 2;

QY 1 HEHAKTSLSSWKHD-----ODMANVSNMFTS--NGKLRVGIYRRNADICSRHRTVSA 51
 ID 114 TGVWTEQAOQNRADICGIVYHRSRDAQAGVANGVADITAIKRLSDMGKVTYTGGLA 173
 Db 55 LODDOLWCLMRTI 66
 174 LEDLPLFKGIP 185

DB 60 NEFHGAMTQDEKHDIAHYANPDNPHVNGXYKAVPGRKAVESFCYLPDPEGDPHTAA 119
 QY 52 GLTLDOLW 61
 Db 120 GTPMHEVLM 129

RESULT 8
 ID Y108_CHLTR STANDARD: PRT: 251 AA.
 AC 084110;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protein CT108.
 GN CT108.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/37/CX;
 RA MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759 (1998).
 CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIP3) FAMILY
 CC -----
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 CC -----
 CC EMBL: AE001284; AAC67699.1; -;
 CC DR PIR: A29894; A29894.
 CC DR InterPro: IPR002678; DUF34.
 CC Pfam: PF01784; DUF34; 1.
 CC TRGFAMS: TRGR00486; DUF34; 1.
 CC KW Complete proteome.
 CC SQ SEQUENCE 251 AA; 27474 MW; A4C2F6BE7517298E CRC64;

Query Match 15.7%; Score 58.5; DB 1; Length 251;
 Best Local Similarity 26.0%; Pred. No. 4.9;
 Matches 19; Conservative 10; Mismatches 23; Indels 21; Gaps 3;

QY 2 EAHKTSLSWK--HDDMANVSNMFTSNGKLRVKG-----YYRNADIC 43
 ID 102 DAHTTGNMKVARDLGWOLSEFSSQPSLGVKGFPEMEVHDFISQLSATYQTPVLAK 161
 Db 44 ---SRHRTSAGL 53
 Db 162 ALGKKRVSSAAL 174

RESULT 9
 ID IL1B-TRIVU STANDARD: PRT: 269 AA.
 AC Q9XS77;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 beta precursor (IL-1 beta).
 GN IL1B.
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;

```

RN [1] SEQUENCE FROM N.A.
RP MEDLINE=99221044; PubMed-10206203;
RX Medlock D.N., Goh L.P., Parlane N.A., Buddle B.M.:
RA "Molecular cloning and physiological effects of brushstall possum
interleukin-1beta ";
RL Interimunol. Immunopathol. 67:359-372(1999).
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDICING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYOGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC CC
CC -I- SUBUNIT: MONOMER.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC CC
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC CC
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CC -----
CC DR EMBL: AF071539; MAD21871.1; -.
CC DR HSSP: P01584; 1H1B.
CC DR InterPro: IPR002348; IL1_HBGF.
CC DR InterPro: IPR003502; IL1_propep.
CC DR InterPro: IPR009795; Interleukin_1.
CC DR Pfam: PF00340; IL1; 1.
CC DR Pfam: PF02394; IL1_HBGF; 1.
CC DR PRINTS: PR00262; IL1HBGF.
CC DR ProDom: PD002536; Interleukin_1; 1.
CC DR SMART: SM00125; IL1; 1.
CC DR PROSITE: PS00253; INTERLEUKIN_1; 1.
CC DR CytoKine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC FT PROPEP 1 112 BY SIMILARITY.
CC KW CYCLOPEP 1 112 INTERLEUKIN-1 BETA.
CC FT CHAIN 113 269
CC SO SEQUENCE 269 AA; 31141 MW; 307A1F5B627D6E7 CRC64;
Query Match 15.7%; Score 58.5; DB 1; Length 269;
Best Local Similarity 24.5%; Pred. No. 5.3;
Matches 23; Conservative 12; Mismatches 28; Indels 31; Gaps 5
QY 1 HEAKT-----SISSMKH-----DOMANYSNMTFSNGKLRYGVGYRRADI--- 42
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 62 HQHQYMWIVVAIEKKKHLNGLSSOPFOONDAIMFTNIPOE-----EPITFKNCDIYES 116
QY 43 -CSHRVTSAGLTLDPLQLWC-----NLRIIH 68
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 117 DSSEIRLYVSODCTIIDIKNCKALSKASSELRALH 150
RESULT 10
ID YRAN HAEIN STANDARD; PRT; 119 AA.
AC PA5300:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Hypothetical protein H11656.
GN H11656.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxId=727;
RN [1]

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RP      SEQUENCE FROM N.A.
RX      STRAIN-Rd / KW20 / ATCC 51907;
RX      MEDLINE=95350630; PubMed=7542800;
RA      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA      Kellerauge A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA      McInney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA      Scott J.D., Shiley R., Liu L.-I., Glodet A., Kelley J.M.,
RA      Weidman J.F., Phillips C.A., Spilgus T., Hedblom E., Cotton M.D.,
RA      Uettermann J.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA      Fine L.D., Fleischmann J.L., Fuhmann J.L., Geoghagen N.S.M.,
RA      Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA      Venter J.C.;
RT      "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL      Rd."
RL      Science 269:496-512(1995).
CC      -I- SIMILARITY: BELONGS TO THE UPF0102 FAMILY. STRONG, TO E.COLI YRAN.
CC      CC
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CC      -----
CC      CCG      EMBL; U32838; AAC23300.1; -
CC      DR      TIGR; H11656; -
CC      DR      InterPro: IPR003509; UPF0102.
CC      DR      Pfam: PF02021; UPF0102; 1.
CC      DR      TIGRFAMs: TIGR00252; TIGR00252; 1.
CC      DR      KW      Hypothetical protein: Complete proteome.
CC      SQ      SEQUENCE 119 AA; 13812 MW; B7359D8181F31AE7 CRC64;
CC      -----
QY      Query Match 15.54; Score 58; DB 1; Length 119;
QY      Best Local Similarity 23.88; Pred. No. 2,3;
QY      Matches 15; Conservative 15; Mismatches 23; Indels 10; Gaps 3;
DB      59 Q1W 61
DB      112 Q-W 113
DB      112 Q-W 113

RESULT 11
DISK_AGRH STANDARD; PRT; 478 AA.
ID DISK_AGRH
AC P30403;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemorrhagic protein-rhodostomin precursor (EC 3.4.24.-) (RHO
DE [contains: Disintegrin rhodostomin]).
DE RHO.
GN Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OC NCHI_TaxID=8717;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RC MEDLINE=95277962; PubMed=7916635;
RX Au L.-C.;
RA "Nucleotide sequence of a full-length cDNA encoding a common
RA precursor of platelet aggregation inhibitor and hemorrhagic protein
RT from Calloselasma rhodostoma venom."
RT Biochim. Biophys. Acta 1173:243-245(1993).
RN [2]
RN SEQUENCE OF 77-478 FROM N.A.
RP TISSUE=Venom gland;
RP TISSUE=Venom gland;

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[illegible]

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FT      DISULFID      345      353      BY SIMILARITY.
FT      DISULFID      411      426      BY SIMILARITY.
FT      DISULFID      413      421      BY SIMILARITY.
FT      DISULFID      420      443      BY SIMILARITY.
FT      DISULFID      434      440      BY SIMILARITY.
FT      DISULFID      439      464      BY SIMILARITY.
FT      DISULFID      452      471      BY SIMILARITY.
FT      SITE           456      458      CELL ATTACHMENT SITE.
FT      CARBOHYD      279      279      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      369      369      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      478 AA; 54006 MW; 6490A2B171D3A830 CRC64;

Query Match
Best Local Similarity 15.4%; Score 57.5; DB 1; Length 478;
Matches 17; Conservative 19; Mismatches 24; Indels 23; Gaps

QY      9      SSNMKHOODAMANSNMTFSNG-KLRVKGIIYRNADICSR-----HRYTSA----- 51
DB      172      TWMEDEPRKKSQSLNLEIKRHVDIVVYDSRCTKHSNDLEVIKRFHEVNAIIIS 231
QY      52      -----GLTLDLQLMCNLRITH 68
DB      232      YKMHGICISLVLETWCGNDLIN 254

RESULT 12
RNI4_YEAST
ID      RNI4_YEAST      STANDARD;      PRT;      677 AA.
AC      P25298;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      mRNA 3'-end processing protein RNI4.14.
GN      RNI4 OR YMR061W OR YMR9796.14.
OS      Saccharomyces cerevisiae (Baker's Yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RN      [1]
RN      RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 28583 / FL100;
RX      MEDLINE=91246175; PubMed=1674817;
RA      Minyelle-Sebastia L., Winsor B.,
RT      "Mutations in the yeast RNI4 and RNI4 genes result in an abnormal
RT      mRNA decay rate; sequence analysis reveals an RNA-binding domain in
RT      the RNI4 protein."
RL      Mol. Cell. Biol. 11:3075-3087(1991).
RN      [2]
RN      RP      REVISIONS.
RC      STRAIN=ATCC 28583 / FL100;
RA      Bonneaud N.;
RN      [3]
RN      Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RP      SEQUENCE FROM N.A.
RC      STRAIN=S288c / AB972;
RA      Devlin K., Churcher C.M., Barrell B.G., Rastrand M.A.;
RN      Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN      [4]
RN      RP      FUNCTION.
RX      MEDLINE=95084159; PubMed=7992054;
RA      Minyelle-Sebastia L., Preker P.J., Keller W.;
RT      "RNI4 and RNI4 proteins as components of a yeast pre-mRNA 3'-end
RT      processing factor."
RT      Science 266:1702-1705(1994).
CC      -1- FUNCTION: COMPONENT OF THE CLEAVAGE FACTOR I (CF I) INVOLVED IN
CC      PRP-mRNA 3'-END PROCESSING. INTERACTS WITH FIP1 AND PROBABLY ALSO
CC      WITH RNI45.
CC      -1- SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC.
CC      -1- SIMILARITY: CONTAINS 6 HAT REPEATS.
CC      -----
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 CC -----
 DR EMBL: M73461; AAA21300.1; -;
 DR EMBL: Z48703; CA89771.1; -;
 DR PIR: A40257; A40257.
 DR SGD: S0004665; RNA14.
 DR InterPro: IPR003107; HAT.
 DR SMART: SM00386; HAT; 3.
 KW mRNA processing; Nuclear protein; Repeat.
 FT REPEAT 56 88 HAT 1.
 FT REPEAT 90 124 HAT 2.
 FT REPEAT 138 170 HAT 3.
 FT REPEAT 181 214 HAT 4.
 FT REPEAT 257 289 HAT 5.
 FT REPEAT 298 330 HAT 6.
 SQ SEQUENCE 677 AA; 79960 MW; 102433295FE7CD63 CRC64;
 Query Match 15.4%; Score 57.5; DB 1; Length 677;
 Best Local Similarity 30.6%; Pred. No. 21;
 Matches 15; Conservative 9; Mismatches 20; Indels 5; Gaps 1;
 QY 15 QDMANVSMFTSNGKRYKGIYYRNADICSRHRYTSAGLTLDIOLMCN 63
 DB 239 QEWLVN-----TNGIKRASPINTLRANKKNIPQGTSDSNIQOLQIWLN 282
 RESULT 13
 ID RPL_HUMAN STANDARD; PRT; 2156 AA.
 AC P56715;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Oxygen-regulated protein 1 (retinitis pigmentosa Rpl protein)
 DE (retinitis pigmentosa 1 protein).
 GN RPL OR ORPL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS HIS-872; TYR-985; THR-1670; PRO-1691
 RP AND TYR-2033.
 RC TISSUE=Retina;
 RX MEDLINE=99318096; PubMed=10391212;
 RA Sullivan L.S., Heckenlively J.R., Bowne S.J., Zuo J., Hide W.A.,
 RA Gal A., Denton M., Inglehearn C.F., Blanton S.H., Dalgner S.P.;
 RT "Mutations in a novel retina-specific gene cause autosomal dominant
 RT retinitis pigmentosa.";
 RL Nat. Genet. 22:255-259(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=99318095; PubMed=10391211;
 RA Pierce E.A., Quinn T., Meenan T., McGee T.L., Berson E.L., Dryja T.P.;
 RT "Mutations in a gene encoding a new oxygen-regulated photoreceptor
 RT protein cause dominant retinitis pigmentosa.";
 RL Nat. Genet. 22:248-254(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99310563; PubMed=10401003;
 RA Guillonneau X., Pirliev N.I., Danciger M., Kozak C.A., Cideciyan A.V.,
 RA Jacobson S.G., Farber D.B.;
 RT "A nonsense mutation in a novel gene is associated with retinitis
 RT pigmentosa in a family linked to the RPL locus.";
 RL Hum. Mol. Genet. 8:1541-1546(1999).
 CC -1- FUNCTION: COULD HAVE A ROLE IN THE DIFFERENTIATION OF
 CC PHOTORECEPTOR CELLS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN RETINA. NOT EXPRESSED IN HEART,
 CC BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, SPLEEN AND

CC PANCREAS.
 CC -1- DISEASE: DEFECTS IN RPL CAUSE RETINITIS PIGMENTOSA FORM 1 (RPL); A
 CC DISEASE CHARACTERIZED BY CONSTRUCTION OF THE VISUAL FIELDS, NIGHT
 CC BLINDNESS, AND FUNDS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED
 CC WITH TRUNCATED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
 CC PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS.
 CC -1- DATABASE: NAME=Retnet;
 CC NOTE=Retinal information network;
 CC WWW="http://www.sph.uth.tmc.edu/retnet/";
 CC DATABASE: NAME=Mutations of the RPL gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/rplmut.htm".
 CC -----
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 CC -----
 DR EMBL: AF143226; AAD44197.1; -;
 DR EMBL: AF143224; AAD44197.1; JOINED.
 DR EMBL: AF143225; AAD44197.1; JOINED.
 DR EMBL: AF143222; AAD44198.1; -;
 DR EMBL: AF141021; AAD42072.1; -;
 DR EMBL: AF152242; AAD46774.1; -;
 DR EMBL: AF152240; AAD46774.1; JOINED.
 DR EMBL: AF152241; AAD46774.1; JOINED.
 DR EMBL: AF146592; AAD46769.1; -;
 DR GeneW: HGNC:10263; RPL.
 DR MIM: 603937; -;
 DR MIM: 180100; -;
 DR InterPro: IPR003533; DCX.
 DR Pfam: PF03607; DCX; 2.
 DR SMART: SM00537; DCX; 2.
 DR PROSITE: PS50309; DC; 2.
 KW Vision; Retinitis pigmentosa; Polymorphism; Repeat.
 FT DOMAIN 36 118 DOUBLECORTIN 1.
 FT DOMAIN 154 233 DOUBLECORTIN 2.
 FT DOMAIN 268 273 POLY-SER.
 FT DOMAIN 671 675 POLY-LYS.
 FT DOMAIN 1687 1691 POLY-SER.
 FT VARIANT 872 872 R -> H.
 FT VARIANT 985 985 /FTID=VAR_007810.
 FT VARIANT 1670 1670 /FTID=VAR_007811.
 FT VARIANT 1691 1691 /FTID=VAR_007812.
 FT VARIANT 1691 1691 S -> P.
 FT VARIANT 2033 2033 /FTID=VAR_007813.
 FT VARIANT 2033 2033 C -> Y.
 SQ SEQUENCE 2156 AA; 240659 MW; 55AEDEBCA3DA507 CRC64;
 Query Match 15.4%; Score 57.5; DB 1; Length 2156;
 Best Local Similarity 28.8%; Pred. No. 81;
 Matches 15; Conservative 13; Mismatches 23; Indels 1; Gaps 1;
 QY 6 TSLSMKHDQDMANVSMFTSNGKRYKGIYYRNADICSRHRYTSAGLTLD 57
 DB 666 SSVASKKKKKKRQQAINSRYDQGLATKGIINKKRIYTKGRITKE-MIVDD 716
 RESULT 14
 ID FCGL_MOUSE STANDARD; PRT; 404 AA.
 AC P26151;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE High affinity immunoglobulin gamma FC receptor 1 precursor (FC-gamma

```

DE RI1 (FCRI) (TGG FC receptor 1).
GN FCGR1 OR FCGR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90111035; PubMed=2136886;
RA Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.;
RT "Molecular cloning and expression of the mouse high affinity Fc
RT receptor for IgG.";
RL J. Immunol. 144:371-378(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9216399; PubMed=1531670;
RA Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;
RT "Structure and mapping of the gene encoding mouse high affinity Fc
RT gamma RI and chromosomal location of the human Fc gamma RI gene.";
RL J. Immunol. 148:1570-1575(1992).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN GAMMA. HIGH
CC AFFINITY RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: MACROPHAGE-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
CC -----
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CC -----
DR EMBL: M31314; AAA40056.1; -.
DR PIR: A43511; A43511.
DR PIR: A46480; A46480.
DR HSP: P12319; 1A.S.
DR MGD: MGI:95498; Fcgr1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00410; Ig_Like; 2.
DR SMART: SM00408; IGC2; 1..
DR IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT FT CHAIN 1 24
FT FT SIGNAL 1 24
FT FT CHAIN 25 404
FT FT HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT FT RECEPTOR I.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 298 320
FT FT POTENTIAL.
FT FT DOMAIN 321 404
FT FT CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 46 102
FT FT IG-LIKE C2-TYPE DOMAIN 1.
FT FT DOMAIN 127 184
FT FT IG-LIKE C2-TYPE DOMAIN 2.
FT FT DOMAIN 214 276
FT FT IG-LIKE C2-TYPE DOMAIN 3.
FT FT DISULFID 53 95
FT FT BY SIMILARITY.
FT FT DISULFID 134 177
FT FT BY SIMILARITY.
FT FT DISULFID 221 269
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 28 48
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 69 69
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 168 168
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 249 249
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 404 AA; 44887 MW; 1CA4F003842767E7 CRC64;

Query Match 15.1%; Score 56.5; DB 1; Length 404;
Best Local Similarity 32.8%; Pred. No. 15;
Matches 22; Conservative 7; Mismatches 11; Indels 27; Gaps 5;
17 WAN--VSNTF--SNGK-----LRVKGIVYRNADICS--RHRVTSAGLT 54

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Db 137 WKNTLVNVTYRNGKSPQFSSDSEVALTKTNLSHSGIYH-----CSGGRHRYTSAGVS 191
OY 55 LODIQLW 61
Db 192 ITVKELF 198

RESULT 15
TRAP_ECOLI ID TRAP_ECOLI STANDARD; PRT; 196 AA.
AC P41068;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TRAP protein.
GN Trap.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Bacteroides.
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94359430; PubMed=7915817;
RA Frost L.S., Ippen-Ihler K., Skurray R.A.;
RT "Analysis of the sequence and gene products of the transfer region of
RT the F sex factor.";
RL Microbiol. Rev. 58:162-210(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / CR63;
RA Shimizu H., Satoh Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.;
RT "Complete nucleotide sequence of the F plasmid: its implications for
RT organization and diversification of plasmid genomes.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: UNKNOWN.
CC -----
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CC -----
DR EMBL: U01159; AAC4193.1; -.
DR DR EMBL: AP001918; BAA97949.1; -.
DR Ecogene; EG40094; trap.
KW Plasmid; Complete proteome.
SQ SEQUENCE 196 AA; 21961 MW; 0197355516942160 CRC64;

Query Match 15.0%; Score 56; DB 1; Length 196;
Best Local Similarity 30.2%; Pred. No. 7.4;
Matches 16; Conservative 10; Mismatches 23; Indels 4; Gaps 2;
OY 17 WANVNMFTSNKTLRVKGI-YRNADICSRHRTSAGLTLODLQMLCNRIIH 68
OY 81 WFSSTD---SSGRSLIGICHYRNADADYVRETDRSLMGIWATLAWIATLAW 130
Db 81 WFSSTD---SSGRSLIGICHYRNADADYVRETDRSLMGIWATLAWIATLAW 130

Search completed: December 8, 2002, 19:31:29
Job time : 15.7226 secs

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 8, 2002, 19:27:28 ; Search time 22.8129 Seconds
(without alignments)
286.555 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEHKTSLSSWKHDQMANV.....TSAGLTLDLQGLMCNLRITH 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR-73:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	18.0	296	2 E72203	conserved hypothet
2	67	18.0	307	2 T46103	hypothetical prote
3	64.5	17.3	276	2 E96990	probable glucanor
4	63.5	17.0	263	1 S31323	orotidine-5'-phosp
5	63.5	17.0	813	2 F83476	probable sideropho
6	61	16.4	1101	2 T20881	hypothetical prote
7	60	16.1	274	2 AC1866	hypothetical prote
8	60	16.1	283	2 AT2835	glycosyl hydrolase
9	60	16.1	354	2 C97614	hypothetical 32.0K
10	59.5	16.0	216	2 S56421	probable hexulose-
11	59.5	16.0	216	2 D91275	probable hexulose-
12	59.5	16.0	216	2 D86116	probable hexulose-
13	59.5	16.0	329	2 A29894	isopenicillin N sy
14	59.5	16.0	427	2 F83984	acetylornithine de
15	59	15.8	187	2 T15023	hypothetical prote
16	58.5	15.7	91	2 T29796	hypothetical prote
17	58.5	15.7	251	2 C71557	probable ACR - Chl
18	58	15.5	119	2 C64174	hypothetical prote
19	58	15.5	330	2 C71096	probable modificat
20	58	15.5	466	2 T02643	hypothetical prote
21	57.5	15.4	478	2 J01301	hemorrhagic protei
22	57.5	15.4	677	2 S54561	RNA14 protein - ye
23	57.5	15.4	729	2 A97747	oligopeptidase B (
24	57.5	15.4	1063	2 S18211	hypothetical prote
25	57	15.3	345	2 D97407	hypothetical prote
26	57	15.3	345	2 AE2625	conserved hypothet
27	57	15.3	398	2 AC1998	hypothetical prote
28	56.5	15.1	216	2 AB1052	probable hexulose-
29	56.5	15.1	280	2 I55577	Fc gamma (19c) rec

30	56.5	15.1	404	2 A46480	Fc gamma (19c) rec
31	56.5	15.1	920	2 C96831	hypothetical prote
32	56.5	15.1	2167	2 T34395	hypothetical prote
33	56	15.0	350	2 S70135	hypothetical prote
34	56	15.0	484	2 S43737	protein kinase SLT
35	56	15.0	785	2 S73098	antipeptidase (EC
36	56	15.0	788	2 AF0122	probable membrane
37	56	15.0	1327	2 B90674	AldA-I adhesin-1lk
38	56	15.0	1349	2 E85524	probable beta-bar
39	55.5	14.9	148	2 T1BH	trypsin inhibitor
40	55.5	14.9	326	2 T09366	Fc gamma (19c) rec
41	55.5	14.9	469	2 T09366	cytochrome P450 ho
42	55.5	14.9	679	2 A40351	adhesion-type prot
43	55.5	14.9	680	2 S17982	kallimann syndrome
44	55.5	14.9	760	2 T06291	extensin homolog T
45	55.5	14.9	837	2 T12531	hypothetical prote

ALIGNMENTS

RESULT 1

E72203 conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: E72203

R:Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; PMID:99287316; PMID:10360571

A:Accession: E72203

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-296 <ARN>

A:Cross-references: GB:AE001822; GB:AE000512; NID:94982429; PIDN:AAD36914.1; PID:9498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1852

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1107

Query Match

Best Local Similarity 27.3%; Pred. No. 2.2;

Matches 15; Conservative 11; Mismatches 19; Indels 10; Gaps 3;

QY 14 DDDM---ANVSNMTFSGKLRVKG---IYRRNADICSRHRVTSAGLTLDLQMC 62

DB 244 EDMEKFGGVPNVFSDAMIEYGYVYGADNC---IALATIPVEKVMKC 294

RESULT 2

T46103 hypothetical protein T25B15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46103

R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Maché, R.; Mewes, H.W.; Lemcke, K.; Mayer,

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23021

A:Accession: T46103

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-307 <ALC>

A:Cross-references: EMBL:AL132972

A:Experimental source: cultivar Columbia; BAC clone T25B15

C:Genetics:

A:Map position: 3

A:Introns: 63/3; 225/2; 267/3

A:Note: T25B15.100

Query Match

18.0%; Score 67; DB 2; Length 307;

Best Local Similarity 18.3%; Pred. No. 2.3;
Matches 15; Conservative 19; Mismatches 26; Indels 22; Gaps 2;

OY 1 HEHNRKSLSSMKHDDOM-----ANVSMTFSNGKLRVKGIIYRN 39

DB 149 HDYKVLSEIWRINKMKRSEHHVVLVGARTSMKTKOCHIHLPYSOG-ITINGVLVYG 207

OY 40 ADICSRHRYTSAGLTLODLQ 61
DB 208 AWTDDKCVLMSFDTSEDEYGVW 229

RESULT 3

E96990 Probable glucanotransferase (endo alpha-1,4 polygalactosaminidase related protein) [imp]

C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C/Accession: E96990

R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C10

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: E96990

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-276 <KUR>

A/Cross-references: GB:AE001437; PIDN:AAK78712.1; PID:Q15023617; GSPDB:GN00168

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Gene: CAC0736

Query Match

Best Local Similarity 17.3%; Score 64.5; DB 2; Length 276;
Pred. No. 4.1;

Matches 18; Conservative 15; Mismatches 15; Indels 11; Gaps 4;

OY 10 SMKHHDDANVSNMFFSN-----GK-LRVKGI---YYRNADICSRHRYTSAGLTLODL 58

DB 105 NWK-DESWIDVSNLKMWDVYVNTGKLNKNGVDGFLDNLDVYSKYKXSMFICLILNI 162

RESULT 4

S31323 orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (*Pichia angusta*)

C/Species: *Pichia angusta*

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000

C/Accession: S31323

R/Merckelbach, A.; Goedecke, S.; Janowicz, Z.A.; Hollenberg, C.P.

submitted to the EMBL Data Library, November 1992

A/Description: Cloning and sequencing of the URA3 locus of the methylotrophic yeast *Hans*

A/Reference number: S31323

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-263 <MER>

A/Cross-references: EMBL:X69461; NID:92783; PIDN:CAAA4221.1; PID:92784

C/Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylase

C/Keywords: carbon-carbon lyase; carboxy-lyase

F/3-26/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>

Query Match

Best Local Similarity 17.0%; Score 63.5; DB 1; Length 263;
Pred. No. 5.1;

Matches 17; Conservative 7; Mismatches 12; Indels 7; Gaps 2;

OY 14 DQMANVSNMFFSNGKLRVKGIIYRN---ADICSRHRYTSAGL 53

DB 90 DRKFADIGNTV---KLYRGKGIYRTSKMADITNAHGVTGAGI 128

RESULT 5

F83476

Probable siderophore receptor PA1365 [Imported] - *Pseudomonas aeruginosa* (strain PA01)

C/Species: *Pseudomonas aeruginosa*

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C/Accession: F83476

R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F83476

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-813 <STO>

A/Cross-references: GB:AE004565; GB:AE004091; NID:99947294; PIDN:AAQ04754.1; GSPDB:GN

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA1365

Query Match

Best Local Similarity 17.0%; Score 63.5; DB 2; Length 813;
Pred. No. 19;

Matches 19; Conservative 11; Mismatches 23; Indels 13; Gaps 3;

OY 6 TSLSMKHDDANVSNMFFSNGK-LRVKGI-----YYRNADICSRHRYT---SAG 52

DB 711 TAYLQYKPPADNMNRLOATFFDSKQYRLDGVSESGRRQVSTYTVDLVSQYRTTPDDQLS 770

OY 53 LRLQDL 58

DB 771 LGIQNL 776

RESULT 6

T20881 hypothetical protein T25E12.4a - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000

C/Accession: T20881; T25282; T26254; T27354

R/Steward, C.

submitted to the EMBL Data Library, March 1997

A/Reference number: T20881

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1101 <NTL>

A/Cross-references: EMBL:T292967; PIDN:CAB07478.1; GSPDB:GN00023; CESP:T25E12.4a

A/Experimental source: clone F14D1

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1101 <NT2>

A/Cross-references: EMBL:T26252; PIDN:CAB04830.1; GSPDB:GN00023; CESP:T25E12.4a

A/Experimental source: clone T25E12

R/Barlow, K.

submitted to the EMBL Data Library, January 1998

A/Reference number: T26254

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1101 <NT4>

A/Cross-references: EMBL:AL021572; PIDN:CAAI6519.1; GSPDB:GN00023; CESP:T25E12.4a

A/Experimental source: clone W06H3

R/Steward, C.

submitted to the EMBL Data Library, January 1998

A/Reference number: T27354

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1101 <NT4>

A/Cross-references: EMBL:AL021507; PIDN:CAAI6430.1; GSPDB:GN00023; CESP:T25E12.4a

A/Experimental source: clone T70C5D

C/Genetics:

C;Gene: Lys

Cineywood

Cineywood

Query Match 16.0%; Score 59.5; DB 2; Length 216;
Best Local Similarity 23.6%; Pred. No. 12;
Matches 17; Conservative 16; Mismatches 28; Indels 11; Gaps 3;

OY 6 TSLSSWKHDDW--ANVSNMTFSNGK-LRVKGIYRNADICSRHRYT-----SAGLT 54
DB 114 TGYTWEOAQOVRDAGIOQVYHRSRDAQAGVAMGEADITAIKRLSDMGFKYVTGGTA 173
OY 55 LODLOLWMCNLR 66
DB 174 LEDLPLFKGIPI 185

RESULT 11

D91275
Probable hexulose-6-phosphate synthase [imported] - Escherichia coli (strain O157:H7, serotype O157:H7)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
DNA Res. 8, 11-22, 2001
A:Reference number: A39623; MUID:21156231; PMID:11258796
A:Accession: D91275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <STO>
A:Cross-references: GB:BA000007; PIDN:BAH38595.1; PID:g13364649; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC5172
C:Superfamily: hypothetical protein H11024

Query Match 16.0%; Score 59.5; DB 2; Length 216;
Best Local Similarity 23.6%; Pred. No. 12;
Matches 17; Conservative 16; Mismatches 28; Indels 11; Gaps 3;

OY 6 TSLSSWKHDDW--ANVSNMTFSNGK-LRVKGIYRNADICSRHRYT-----SAGLT 54
DB 114 TGYTWEOAQOVRDAGIOQVYHRSRDAQAGVAMGEADITAIKRLSDMGFKYVTGGTA 173
OY 55 LODLOLWMCNLR 66
DB 174 LEDLPLFKGIPI 185

RESULT 12

D86116
Probable hexulose-6-phosphate synthase sgah [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074933; PMID:11206551
A:Accession: D86116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <STO>
A:Cross-references: GB:AE005174; NID:g12519187; PIDN:AAG59392.1; GSPDB:GN00145; UNCP:458
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: sgah
C:Superfamily: hypothetical protein H11024

Query Match 16.0%; Score 59.5; DB 2; Length 216;
Best Local Similarity 23.6%; Pred. No. 12;
Matches 17; Conservative 16; Mismatches 28; Indels 11; Gaps 3;
OY 6 TSLSSWKHDDW--ANVSNMTFSNGK-LRVKGIYRNADICSRHRYT-----SAGLT 54

DB 114 TGYTWEOAQOVRDAGIOQVYHRSRDAQAGVAMGEADITAIKRLSDMGFKYVTGGTA 173
OY 55 LODLOLWMCNLR 66
DB 174 LEDLPLFKGIPI 185

RESULT 13

A29894
Isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces clavuligerus
C:Species: Streptomyces clavuligerus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 26-May-2000
R:Leskiy, B.K.; Aharonowitz, Y.; Meyerech, M.; Wolfe, S.; Vining, L.C.; Westlake, D.W.
Gene 62, 187-196, 1988
A:Title: Cloning and nucleotide sequence determination of the isopenicillin N synthet
A:Reference number: A29894; MUID:88212175; PMID:3130293
A:Accession: A29894
A:Molecule type: DNA
A:Residues: 1-329 <LES>
A:Cross-references: GB:M19421; NID:g153328; PIDN:AAA26770.1; PID:g153329
C:Superfamily: isopenicillin N synthase
A:Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreduct
F:48, 212,268/Binding site: Iron (His) #status predicted

Query Match 16.0%; Score 59.5; DB 2; Length 329;
Best Local Similarity 25.7%; Pred. No. 20;
Matches 18; Conservative 10; Mismatches 33; Indels 9; Gaps 2;

OY 1 HEAHTSLSSWKHD-----ODMANSMTFS--NGKLRVGIYRNADICSRHRYTSA 51
DB 60 NEFGATMDERKDHDLIAHNPDPNPHVNGYKAVGKRAVSEFCYLPNDPGEHPIPTAA 119
OY 52 GLTFLODLW 61
DB 120 GTPMHEVNLN 129

RESULT 14

F83984
acetylornithine deacetylase BH2678 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512562; PMID:11058132
A:Accession: F83984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <STO>
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06397.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2678
C:Superfamily: succinyl-diaminopimelate desuccinylase

Query Match 16.0%; Score 59.5; DB 2; Length 427;
Best Local Similarity 29.9%; Pred. No. 27;
Matches 20; Conservative 7; Mismatches 35; Indels 5; Gaps 2;

OY 2 EAHKTSLSWKHDDW--ANVSNMTFSNGKLRVKGIIYRNADICSRHRYTSAGLTLDL 58
DB 361 EERVKTSMSQYTDGWLAEAGIPITLFGPKLDAHSVNEELIAELVYVYTLTLTF--I 418
OY 59 QLMCNLR 65
DB 419 YEMCHLR 425

RESULT 15

T15023
hypothetical protein Y1108 - Yersinia pestis plasmid pMT1
C:Species: Yersinia pestis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T15023; T14697
R:Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A:Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
A:Reference number: Z18268; MIMD:99043898; PMID:9826348
A:Accession: T15023
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-187 <LIN>
A:Cross-references: EMBL:AF074611; NID:93883003; PID:93883106; PIDN:AAC82766.1
R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garne, J.; Kobayashi, A.; Carrano,
submitted to the EMBL data library, March 1998
A:Description: Structural organization of virulence determinants in three Yersinia pestis
A:Reference number: Z18168
A:Accession: T14697
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-187 <HUP>
A:Cross-references: EMBL:AF053947; NID:92996286; PID:92996333; PIDN:AAC13213.1
C:Genetics:
A:Gene: Y1108
A:Genome: plasmid pMT1
C:Superfamily: Yersinia pestis plasmid pMT1 hypothetical protein Y1108

Query Match 15.88; Score 59; DB 2; Length 187;
Best Local Similarity 37.18; Pred. No. 12;
Matches 13; Conservative 7; Mismatches 9; Indels 6; Gaps 1;

QY 16 DMANVSMTFSNGKLRVKGIVRRADICSRHRYTS 50
DB 124 DMADVAMWLEANGRLK-----ENAEIAHNAHYLS 152

Search completed: December 8, 2002, 19:34:47
Job time : 26.8129 secs

Tue Dec 10 10:51:45 2002

us-09-880-457-4_copy_20_87.ra1

Page 1

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 8, 2002, 19:30:43 : Search time 14.4774 Seconds
(without alignments)
138.199 Million cell updates/sec

Title: US-09-880-457-4_COPY_20_87
Perfect score: 373
Sequence: 1 HEAKRTSLSSMKHQDQWANY.....TSAGLTLDLQMCNRIITH 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/laa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/laa/5A.COMB.pep:*
4: /cgn2_6/ptodata/1/laa/5B.COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCMTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/laa/backfile1.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	47.7	317	3 US-08-996-139-13	Sequence 13, Appl
2	178	47.7	317	4 US-08-995-659-13	Sequence 13, Appl
3	178	47.7	317	4 US-09-215-649A-13	Sequence 4, Appl
4	178	47.7	317	4 US-09-052-521C-4	Sequence 13, Appl
5	178	47.7	317	4 US-09-577-780-13	Sequence 11, Appl
6	172	46.1	294	4 US-08-995-658-11	Sequence 11, Appl
7	172	46.1	294	4 US-09-215-649A-11	Sequence 11, Appl
8	172	46.1	294	4 US-09-577-780-11	Sequence 11, Appl
9	172	46.1	316	2 US-08-842-842-7	Sequence 7, Appl
10	172	46.1	316	4 US-08-989-362-2	Sequence 2, Appl
11	172	46.1	316	4 US-09-052-521C-2	Sequence 2, Appl
12	172	46.1	316	4 US-09-052-521C-34	Sequence 34, Appl
13	172	46.1	316	4 US-08-594-031-100	Sequence 100, App
14	172	46.1	316	4 US-08-594-031-102	Sequence 102, App
15	172	46.1	316	4 US-09-413-231-5	Sequence 9, Appl
16	172	46.1	316	4 US-09-413-231-9	Sequence 9, Appl
17	172	46.1	316	4 US-09-052-521C-33	Sequence 33, Appl
18	172	46.1	316	4 US-08-332-562A-93	Sequence 93, Appl
19	172	46.1	316	4 US-08-618-911-6	Sequence 6, Appl
20	172	46.1	316	4 US-08-211-430-2	Sequence 2, Appl
21	172	46.1	316	4 US-08-761-136-1	Sequence 1, Appl
22	172	46.1	316	4 US-09-413-231-10	Sequence 10, Appl
23	172	46.1	316	4 US-08-472-240A-20	Sequence 20, Appl
24	172	46.1	316	4 US-09-257-490-12	Sequence 12, Appl
25	172	46.1	316	4 US-07-956-483-15	Sequence 15, Appl
26	172	46.1	316	4 US-07-956-483-15	Sequence 15, Appl
27	172	46.1	316	4 US-08-996-139-13	Sequence 13, Appl

28	54	14.5	146	4 US-08-637-323-1	Sequence 1, Appl
29	54	14.5	149	3 US-08-584-031-16	Sequence 16, Appl
30	54	14.5	151	1 US-07-940-605A-3	Sequence 3, Appl
31	54	14.5	151	1 US-08-690-096-3	Sequence 3, Appl
32	54	14.5	261	1 US-07-940-605A-2	Sequence 2, Appl
33	54	14.5	261	1 US-08-184-422-8	Sequence 8, Appl
34	54	14.5	261	1 US-08-360-923A-2	Sequence 2, Appl
35	54	14.5	261	1 US-08-446-922-4	Sequence 4, Appl
36	54	14.5	261	2 US-08-431-055-4	Sequence 4, Appl
37	54	14.5	261	2 US-08-690-096-2	Sequence 2, Appl
38	54	14.5	261	2 US-08-249-189-12	Sequence 12, Appl
39	54	14.5	261	2 US-08-484-624A-12	Sequence 12, Appl
40	54	14.5	261	2 US-08-477-733B-12	Sequence 12, Appl
41	54	14.5	261	3 US-08-763-995-2	Sequence 2, Appl
42	54	14.5	261	3 US-09-088-913A-12	Sequence 12, Appl
43	54	14.5	261	3 US-08-589-771B-8	Sequence 8, Appl
44	54	14.5	261	4 US-08-769-819-12	Sequence 12, Appl
45	54	14.5	261	4 US-08-770-974-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-996-139-13
: Sequence 13, Application US/08996139
: Patient No. 6017729
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/996,139
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 317 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-996-139-13

Query Match 47.7% Score 178; DB 3; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSKRDHODMANNMTEFSGKLRV--GIYYRNADICSRHRTVSGTLQDLOL 60
DB 179 SHKVSLSWYHDKGMAKISNMTEFSGKLIYNODGYIYXNICRHHETSGDLATEYLQ 238

RESULT 2

US-08-995-659-13
Sequence 13, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION NUMBER: US/08/995 659
FILING DATE: 22 DECEMBER 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-995-659-13

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSKRDHODMANNMTEFSGKLRV--GIYYRNADICSRHRTVSGTLQDLOL 60
DB 179 SHKVSLSWYHDKGMAKISNMTEFSGKLIYNODGYIYXNICRHHETSGDLATEYLQ 238

RESULT 3
US-09-215-649A*13

Sequence 13, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <unknown>

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSKRDHODMANNMTEFSGKLRV--GIYYRNADICSRHRTVSGTLQDLOL 60
DB 179 SHKVSLSWYHDKGMAKISNMTEFSGKLIYNODGYIYXNICRHHETSGDLATEYLQ 238

RESULT 4

US-09-052-521C-4
Sequence 4, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:

APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23

PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16

NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4

Tue Dec 19 10:51:45 2002

us-09-880-457-4_copy_20_87.ra1

Page 3

LENGTH: 317
TYPE: PRT
ORGANISM: Human
US-09-052-521C-4

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2,6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHODMANVSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLDDLOL 60
DB 179 SHKVSLSWYHDRGAKISNMTFSGKLRVNDGFYLYANICFRHHTSGDGLATEYLQL 238

RESULT 5
US-09-577-780-13
Sequence 13, Application US/09577780
Patent No. 6419929

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

Query Match 47.7% Score 178; DB 4; Length 317;
Best Local Similarity 60.0%; Pred. No. 2,6e-15;
Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHODMANVSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLDDLOL 60
DB 179 SHKVSLSWYHDRGAKISNMTFSGKLRVNDGFYLYANICFRHHTSGDGLATEYLQL 238

RESULT 6

US-08-996-139-11
Sequence 11, Application US/08996139
Patent No. 6017729

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)233-0644
TELEFAX: (206)587-0430

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-996-139-11

Query Match 46.1% Score 172; DB 3; Length 294;
Best Local Similarity 56.7%; Pred. No. 1,5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHODMANVSNMTFSGKLRK--GIYRNADICSRHVTSGAGTLDDLOL 60
DB 156 SHKVSLSWYHDRGAKISNMTLSNGKLRVNDGFYLYANICFRHHTSGSVFTDYLQL 215

RESULT 7
US-08-995-659-11
Sequence 11, Application US/08995659
Patent No. 6242213

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
MARASKOVSKY, Eugene
GALBERT, Laurent

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA

Query Match 46.1% Score 172; DB 3; Length 294;
Best Local Similarity 56.7%; Pred. No. 1,5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-11

Query Match 46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 3 AHKTSLSWKHDQWVANSMTSGNKLRYK--GIYRNADICSRHRVTSAGLTLDLQL 60
DB 156 SHKVTLSWYHDKGMAKISNMTLSNGLRVNQGCFYLVANICFRHHEISGVSPTDYL 215

RESULT 8
US-09-215-649A-11
Sequence 11, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.5e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 3 AHKTSLSWKHDQWVANSMTSGNKLRYK--GIYRNADICSRHRVTSAGLTLDLQL 60
DB 156 SHKVTLSWYHDKGMAKISNMTLSNGLRVNQGCFYLVANICFRHHEISGVSPTDYL 215

RESULT 9
US-09-577-780-11
Sequence 11, Application US/095777780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:


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SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-577-780-11

Query Match      46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTVSAGITLDDIQL 60
Db 156 SHKVTLSWYHDSGMAKISNMTLSNGKLRVNQDGFYLLVLANICFRHHETSGSVPTDYQL 215

RESULT 10
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-842-7

Query Match      46.1%; Score 172; DB 2; Length 316;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTVSAGITLDDIQL 60
Db 178 SHKVTLSWYHDSGMAKISNMTLSNGKLRVNQDGFYLLVLANICFRHHETSGSVPTDYQL 237

RESULT 11
US-08-989-362-2
Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens: Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute

SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-577-780-11

Query Match      46.1%; Score 172; DB 4; Length 294;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTVSAGITLDDIQL 60
Db 156 SHKVTLSWYHDSGMAKISNMTLSNGKLRVNQDGFYLLVLANICFRHHETSGSVPTDYQL 215

RESULT 12
US-09-052-521C-2
Sequence 2, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Bry
CURRENT FILING DATE: 1998-03-30
CURRENT APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2
LENGTH: 316
TYPE: PRT
ORGANISM: Mouse
US-09-052-521C-2

Query Match      46.1%; Score 172; DB 4; Length 316;
Best Local Similarity 56.7%; Pred. No. 1.6e-14;
Matches 34; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

3 AHKTSLSWKHDDQMANVSNMTFSNGKLRVK--GIYYRNADICSRHRTVSAGITLDDIQL 60
Db 178 SHKVTLSWYHDSGMAKISNMTLSNGKLRVNQDGFYLLVLANICFRHHETSGSVPTDYQL 237

RESULT 13
US-08-989-362-2
Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens: Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
```

RESULT 14
US-08-594-031-100
; Sequence 100, Application US/08594031
; Patent No. 5783182
GENERAL INFORMATION

APPLICANT: THOMPSON, Timothy C.
 TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
 NUMBER OF SEQUENCES: 175
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BAKER & BOTTS, L.L.P.
 STREET: 1299 pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004-2400
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/594,031
 FILING DATE: 30-JAN-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/006,838
 FILING DATE: 16-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Remenick, James
 REGISTRATION NUMBER: 36, 902
 REFERENCE/DOCKET NUMBER: 04146-0110
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-639-7700
 TELEFAX: 202-639-7890
 TELEX:
 INFORMATION FOR SEQ ID NO: 100:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 376 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

Query Match	16.9%	Score 63;	DB 1;	Length 376;
Best Local Similarity	22.1%;	Pred. No. 3.1;		
Matches 17; Conservative	16;	Mismatched	20	

RESULT 15
US-08-594-031-102
; Sequence 102, Application US/085404031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:

```

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? COUNTRY: USA
? ZIP: 20004-2400
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ Version 1.5
? CURRENT APPLICATION NUMBER:
? APPLICATION NUMBER: US/08/594,031
? FILING DATE: 30-JAN-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE: 60/006,838
? ATTORNEY/AGENT INFORMATION:
? NAME: Remenick, James
? REGISTRATION NUMBER: 36,902
? REFERENCE/DOCKET NUMBER: 00446-0110
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-639-7700
? TELEFAX: 202-639-7890
?
? INFORMATION FOR SEQ ID NO: 102:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 376 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: NO
? ORIGINAL SOURCE:
? N-terminal
?
US-08-594-031-102

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Query Match 16.9%; Score 63; DB 1; Length 376;
Best Local Similarly 22.1%; Pred. No. 3.1;
Matches 17; Conservative 16; Mismatches 28; Indels 16; Gaps 4.

Tue Dec 19 10:51:45 2002

us-09-880-457-4_copy_20_87.ra1

Page 7

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OY      1 HEAAKTSLS-SWKHDODMAYNS-----NNTFESNG-----KLRVGYITRYNADICSR 45
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      189 HDHSNSTYTKKSGCNTGVSNTHTYNTYVNGTSNTYKKAAGC RSKTS GAADNSRDICNR 248
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      46 H-RVTSAGLLDLDL 61
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: December 8, 2002, 19:35:33
Job time : 16.4774 secs

Tue Dec 10 10:51:43 2002

us-09-880-457-4.ispt

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: December 8, 2002, 18:34:08 ; Search time 57.2516 Seconds
(without alignments)
313.111 Million cell updates/sec

Title: US-09-880-457-4
Perfect score: 1 MALLTSLQILLIPISISH.....TSAGITLQDLQMCNLRIRH 87
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mmc.*
9: sp-organella.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*
15: sp_rviro.*
16: sp_bacteriaph.*
17: sp-archaeop.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	69	15.2	214 13	Q9D25 brachydanio
2	69	15.2	1130 15	Q88282 snakehead r
3	68.5	15.1	1171 17	Q97B7 thermoplas
4	68	14.9	107 10	Q9FGA8 arabidopsi
5	67.5	14.8	491 4	Q43651 homo sapien
6	67.5	14.8	491 4	Q9B56 homo sapien
7	67.5	14.8	491 4	Q9B56 homo sapien
8	67.5	14.8	491 4	Q9B56 homo sapien
9	67.5	14.8	1000 4	Q9B56 homo sapien
10	67.5	14.8	1018 4	Q9B56 homo sapien
11	67.5	14.8	1090 4	Q9B56 homo sapien
12	67.5	14.8	1214 4	Q9B56 homo sapien
13	67	14.7	296 16	Q9X2G7 arabidopsi
14	67	14.7	307 10	Q9X2G7 arabidopsi
15	67	14.7	478 15	Q71146 human immun
16	66.5	14.6	1514 5	Q9NBK9 drosophila

Result No.	Score	Query Length	DB ID	Description
17	66.5	14.6	1514 5	Q9NBK9 drosophila
18	66	14.5	286 10	Q9C6R2 allowyces a
19	65.5	14.4	212 7	Q9G982 ictalurus p
20	65	14.3	131 7	Q46867 arabidopsi
21	65	14.3	210 10	Q49734 fusobacteri
22	65	14.3	364 16	Q8RFS0 oryza sativ
23	65	14.3	621 10	Q9F6N6 streptomyce
24	64.5	14.2	276 16	Q9X6N2 clostridium
25	64.5	14.2	355 17	Q97L30 sulfolobus
26	64.5	14.2	355 17	Q97L30 sulfolobus
27	64.5	14.2	427 16	Q9K9G9 bacillus ha
28	64	14.1	1485 6	Q8NTW4 sepius oe
29	63.5	14.0	156 6	Q8S007 streptomyce
30	63.5	14.0	262 2	Q9VCF9 drosophila
31	63.5	14.0	297 5	Q9VCF9 drosophila
32	63.5	14.0	561 16	Q8YPE8 pseudomonas
33	63.5	14.0	813 16	Q913X9 gallus galli
34	63	13.8	287 13	Q90WT9 agrobacteri
35	63	13.8	345 16	Q8UIA0 salmella sci
36	62.5	13.7	156 6	Q8S008 chlamydomon
37	62.5	13.7	246 8	Q8W109 oryza sativ
38	62.5	13.7	251 10	Q942B1 oryza sativ
39	62.5	13.7	336 3	Q9HDX9 pneumocysti
40	62.5	13.7	439 3	Q9HEX9 rickettsia s
41	62.5	13.7	2353 16	Q8XTZ4 rickettsia s
42	62	13.6	158 17	Q96232 sulfolobus
43	62	13.6	638 10	Q9M393 arabidopsi
44	62	13.6	774 5	Q9VJ73 drosophila
45	62	13.6	774 5	Q9VJ73 drosophila

ALIGNMENTS

Result No.	Score	Query Length	DB ID	Description
1	69	15.2	214 13	Q9D25 brachydanio
2	69	15.2	1130 15	Q88282 snakehead r
3	68.5	15.1	1171 17	Q97B7 thermoplas
4	68	14.9	107 10	Q9FGA8 arabidopsi
5	67.5	14.8	491 4	Q43651 homo sapien
6	67.5	14.8	491 4	Q9B56 homo sapien
7	67.5	14.8	491 4	Q9B56 homo sapien
8	67.5	14.8	491 4	Q9B56 homo sapien
9	67.5	14.8	1000 4	Q9B56 homo sapien
10	67.5	14.8	1018 4	Q9B56 homo sapien
11	67.5	14.8	1090 4	Q9B56 homo sapien
12	67.5	14.8	1214 4	Q9B56 homo sapien
13	67	14.7	296 16	Q9X2G7 arabidopsi
14	67	14.7	307 10	Q9X2G7 arabidopsi
15	67	14.7	478 15	Q71146 human immun
16	66.5	14.6	1514 5	Q9NBK9 drosophila

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RESULT 2
ID 088282 PRELIMINARY: PRT: 1130 AA.
AC 088282;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
EN Envelope protein.
OS Snakehead retrovirus.
OC Viruses; Retrovirdae; Epsilonretrovirus.
NCBI_TaxID=40270;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96211493; PubMed=8648695;
RA Hart D., Frierichs G.N., Rambaut A., Onions D.E.;
RT "Complete nucleotide sequence and transcriptional analysis of
RL snakehead fish retrovirus.";
RN J. Virol. 70:3606-3616(1996).
RP SEQUENCE FROM N.A.
RA Hart D., Frierichs G.N., Rambaut A., Onions D.E.;
RT "Evidence for a new retrovirus genus of piscine origin.";
RL EMBL: U26458; A034858.1;
DR EMBL;
SQ SEQUENCE 1130 AA; 128317 MW; B6A4F8095E4F0D3F CRC64;

Query Match
Best Local Similarity 15.2%; Score 69; DB 15; Length 1130;
Matches 22; Conservative 11; Mismatches 22; Indels 30; Gaps 4;

QY 25 TSLSSWKH-----QDANVSNMTFSGKLRKGIYRRNADICSHRV-----TSA 70
DB 476 SSGNSMKAIKIDIRKOK-----QKCYFSGKLRKGIYRRNADICSHRV-----TSA 70
QY 71 GLTIG-----DLQMCNL 83
DB 532 TKTITGVTWTTAVVKIDLQOWVDI 556

RESULT 3
ID 09787 PRELIMINARY: PRT: 1171 AA.
AC 09787;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DE Hypothetical protein TV0458.
GN TV0458 OR TVG0449104.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GS51 / DSM 4299 / JCM 9571;
RA MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Nunobiki T., Yamamoto Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AP000992; BAB59600.1;
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1.1; UNKNOWN.1.
SQ SEQUENCE 1171 AA; 132418 MW; D347281D857E6BE CRC64;

Query Match
Best Local Similarity 15.1%; Score 68.5; DB 17; Length 1171;
Matches 23; Conservative 17; Mismatches 32; Indels 13; Gaps 4;

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QY 13 LIPSIHSHE---AKTSLSSWKHDQMANVSN-----MTFSGKLRKGIYRRNADIC 62
DB 885 LMEPALGHVYLVNFTYVTKTSWNINNTLYANLSNAPATVYKLSNRDL--NGSYLHI-LA 941
QY 63 SRHRTSAGLTLODLOLMCNIRIIT 87
DB 942 YPKNLTSLVITTINGLRUCEADFIN 966

RESULT 4
ID 09FGA8 PRELIMINARY: PRT: 187 AA.
AC 09FGA8;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE Similarity to pollen-specific protein Bnm1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphorbia; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=COLDWIBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL EMBL: AB026650; BAB10289.1;
DR EMBL;
SQ SEQUENCE 187 AA; 20056 MW; 305781D3A0738AEA CRC64;

Query Match
Best Local Similarity 14.9%; Score 68; DB 10; Length 187;
Matches 22; Conservative 9; Mismatches 26; Indels 10; Gaps 2;

QY 20 HEAH-----KTSLSWKHDQMANVSNMTFSGKLRKGIYRRNADICSHRVTSAGL 72
DB 102 HDAYVGIASLKSRLLEKSDPTANYDVWVGSDPTRRKVGLVKNPTASK---TLNEM 158
QY 73 TLQDLOL 79
DB 159 TLQMEDL 165

RESULT 5
ID 043651 PRELIMINARY: PRT: 491 AA.
AC 043651;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE Shab-related delayed-rectifier K+ channel alpha subunit.
GN KCNS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LENS EPITHELIUM;
RA MEDLINE=99413882; PubMed=10484328;
RA Shepard A.R., Rae J.L.;
RT "Electrically silent potassium channel subunits from human lens
RT epithelium.";
RL Am. J. Physiol. 277:C412-C424(1999).
DR EMBL; AF043472; AAC13164.1;
DR InterPro; IPR000210; BTF_P02.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003971; KV_channel.
DR InterPro; IPR003968; KV_channel.
DR InterPro; IPR003091; K_channel.

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DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF02214; K_tetra.1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01494; KVCHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR SMART: SM00225; BTB; 1.
KW Ionic channel.
FT VARIANT 450 450 A->T.
SQ SEQUENCE 491 AA; 55970 MW; FFF12CA3CDA50185 CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 491;
Best Local Similarity 22.0%; Pred. No. 12;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MATLTSLOILLIPISHEAKTSLSS-----WKHDQMANVSNKTKLRKGIY 55
DB 328 LFLSVGISIFSVLYSVEKDHSTSLTSPICMW-----WATISMTVGYG----- 374
QY 56 YRNADICSRHRTSAGLTLDLQMLNRII 86
DB 375 -----DTHPVTLAKGLIASTCIIGILVY 398

RESULT 6
ID Q96B56 PRELIMINARY; PRT; 491 AA.
AC Q96B56;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015947; AAH15947.1.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF02214; K_tetra.1.
SQ SEQUENCE 491 AA; 56047 MW; 185D80646109C629 CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 491;
Best Local Similarity 22.0%; Pred. No. 12;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MATLTSLOILLIPISHEAKTSLSS-----WKHDQMANVSNKTKLRKGIY 55
DB 328 LFLSVGISIFSVLYSVEKDHSTSLTSPICMW-----WATISMTVGYG----- 374
QY 56 YRNADICSRHRTSAGLTLDLQMLNRII 86
DB 375 -----DTHPVTLAKGLIASTCIIGILVY 398

RESULT 7
ID Q9B031 PRELIMINARY; PRT; 491 AA.
AC Q9B031;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Unknown (protein for MGC:4213) (Potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004987; AAH04987.1.
DR EMBL: BC004148; AAH04148.1.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003969; Kv6_channel.
DR InterPro: IPR003971; Kv9_channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR003973; Shab_channel.
DR InterPro: IPR003974; Shaw_channel.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF02214; K_tetra.1.
DR PRINTS: PR00169; KCHANNEL.
DR PRINTS: PR01492; KVCHANNEL.
DR PRINTS: PR01494; KVCHANNEL.
DR PRINTS: PR01491; KVCHANNEL.
DR PRINTS: PR01495; SHABCHANNEL.
DR PRINTS: PR01498; SHAWCHANNEL.
DR SMART: SM00225; BTB; 1.
SQ SEQUENCE 491 AA; 55984 MW; A5F12BF077A50DAD CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 491;
Best Local Similarity 22.0%; Pred. No. 12;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MATLTSLOILLIPISHEAKTSLSS-----WKHDQMANVSNKTKLRKGIY 55
DB 328 LFLSVGISIFSVLYSVEKDHSTSLTSPICMW-----WATISMTVGYG----- 374
QY 56 YRNADICSRHRTSAGLTLDLQMLNRII 86
DB 375 -----DTHPVTLAKGLIASTCIIGILVY 398

RESULT 8
ID Q9TT17 PRELIMINARY; PRT; 491 AA.
AC Q9TT17;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Voltage-gated delayed-rectifier potassium channel Kv9.3.
OS Oryzotolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryzotolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=CORNEA ENDOTHELIOU;
RA Rae J.L.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF209723; AAF22833.1.
DR InterPro: IPR000210; BTB_POZ.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR003971; Kv9_channel.
DR InterPro: IPR003968; Kv_channel.
DR InterPro: IPR003091; K_channel.
DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M+channel_nlg.
DR Pfam: PF00520; ion_trans.1.
DR Pfam: PF02214; K_tetra.1.

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DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01494; KYCHANNEL.
 DR PRINTS; PR01491; KYCHANNEL.
 DR SMART; SM00225; BTB; 1.
 KW Ionic channel
 SQ SEQUENCE 491 AA; 55941 MW; 2EE396E0889D6F77 CRC64;

Query Match 14.8%; Score 67.5; DB 6; Length 491;
 Best Local Similarity 22.0%; Pred. No. 12;
 Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MAILTSQILLILIPSHAKTSLS-----WKHDQWANYNMTFSNGKLRVAGIY 55
 DB 328 LFLSVGISISVLTYSVEKDHSSLSLIPICW-----WATISMTYVG----- 374
 QY 56 YRNADICSRHRTSAGLTDLDLQMCNLRIT 86
 DB 375 -----DTHPVTLAGKLIASTCIGCIIIV 398

RESULT 9

09UIB9

ID 09UIB9 PRELIMINARY; PRT; 1000 AA.

AC 09UIB9; PRELIMINARY; PRT; 1000 AA.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Bicarbone transporter.
 GN BT.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RX NCBI_TaxId=9606;
 RN [1]

RP SEQUENCE FROM N.A.

RA Romero M.F.

RT "Cloning of a HCO3 transporter, NT2-NBC, from human brain, similar to

RT both the Anion exchangers (Aes) and the Na/Bicarbone cotransporters

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF053755; AAF21720.1; -

DR HSSP; P02730; IBNX.

DR InterPro; IPR001717; Anion-exchange.

DR InterPro; IPR003020; HCO3_cotransp.

DR Pfam; PF00955; HCO3_cotransp. 1.

DR PRINTS; PR01231; HCO3TRANSPO.

DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1000 AA; 112501 MW; 93FMA40A3141F8F7 CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 1000;

Best Local Similarity 31.9%; Pred. No. 27;

Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;

QY 16 PSISHEAKHTSLSSWKHDQWMA-NVS--NMTFSNGKLRVAGIYRNADICSRHRTSAGL 72
 DB 558 PNPSE-----TLQWKKNDITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
 QY 73 TLQDLQMC 81
 DB 606 YIPDVLEWC 614

RESULT 10

060350

ID 060350 PRELIMINARY; PRT; 1018 AA.

AC 060350; PRELIMINARY; PRT; 1018 AA.
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Sodium bicarbonate cotransporter2.
 GN SBC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RX NCBI_TaxId=9606;
 RN [1]

RP SEQUENCE FROM N.A.

RA Ishibashi K., Sasaki S., Marumo F.;

RC TISSUE-RETINA;

RT "Molecular cloning of a new sodium bicarbonate cotransporter cDNA from

RT human retina."

RL Biochem. Biophys. Res. Commun. 0:0-0(1998).

DR EMBL; AB012130; BAA25898.1; -

DR HSSP; P02730; IBNX.

DR InterPro; IPR001717; Anion-exchange.

DR InterPro; IPR003020; HCO3_cotransp.

DR Pfam; PF00955; HCO3_cotransp. 1.

DR PRINTS; PR01231; HCO3TRANSPO.

DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1018 AA; 114204 MW; A3779D9D3A1E30BC CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 1018;

Best Local Similarity 31.9%; Pred. No. 28;

Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;

QY 16 PSISHEAKHTSLSSWKHDQWMA-NVS--NMTFSNGKLRVAGIYRNADICSRHRTSAGL 72
 DB 558 PNPSE-----TLQWKKNDITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 605
 QY 73 TLQDLQMC 81
 DB 606 YIPDVLEWC 614

RESULT 11

09HC88

ID 09HC88 PRELIMINARY; PRT; 1090 AA.

AC 09HC88; PRELIMINARY; PRT; 1090 AA.
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Sodium bicarbonate cotransporter 2b.
 GN NBC2b.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RX NCBI_TaxId=9606;
 RN [1]

RP SEQUENCE FROM N.A.

RA Pushkin A., Abduladze N., Newman D., Hwang J., Kurtz I.;

RT "Homo sapiens sodium bicarbonate cotransporter 2b mRNA, complete

RT cds."

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF089726; AAG16773.1; -

DR HSSP; P02730; IBNX.

DR InterPro; IPR001717; Anion-exchange.

DR InterPro; IPR003020; HCO3_cotransp.

DR Pfam; PF00955; HCO3_cotransp. 1.

DR PRINTS; PR01231; HCO3TRANSPO.

DR TIGRFAMs; TIGR00834; ae; 1.

SQ SEQUENCE 1090 AA; 123080 MW; 541839C9B565896 CRC64;

Query Match 14.8%; Score 67.5; DB 4; Length 1090;

Best Local Similarity 31.9%; Pred. No. 30;

Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;

QY 16 PSISHEAKHTSLSSWKHDQWMA-NVS--NMTFSNGKLRVAGIYRNADICSRHRTSAGL 72
 DB 648 PNPSE-----TLQWKKNDITAHNISWRNLTVSECK-KLRGVFLGSA--CGHH-----GP 695
 QY 73 TLQDLQMC 81
 DB 696 YIPDVLEWC 704

RESULT 12
 Q9Y6M7 PRELIMINARY: PRT: 1214 AA.
 ID Q9Y6M7
 AC Q9Y6M7: 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 21, last annotation update)
 DE Sodium bicarbonate cotransporter 3.
 GN SLC4A7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SKELETAL MUSCLE;
 RC MEDLINE=99278433; PubMed=10347222;
 RC PubMed=99278433; PubMed=10347222;
 RA Pushkin A., Abuladze N., Lee I., Newman D., Hwang J., Kurtz I.;
 RA "Cloning, tissue distribution, genomic organization, and functional
 RA characterization of NBC3, a new member of the sodium bicarbonate
 RA cotransporter family."
 RT J. Biol. Chem. 274:16569-16575(1999).
 RL EMBL: AF047033; AAD38322.1;
 DR HSSP: P02730; IBNX.
 DR Interpro: IPR001717; Anion_exchange.
 DR Interpro: IPR003020; HCO3_cotransp.
 DR Pfam: PF00955; HCO3_cotransp. 1.
 DR PRINTS: PR01231; HCO3TRANSPORT.
 DR TIGR: TIGR00834; ae: 1.
 DR TIGR: TIGR00834; ae: 1.
 SO SEQUENCE 1214 AA; 136042 MW; EF2035005BF5267 CRC64;
 Query Match 14.8%; Score 67.5; DB 4; Length 1214;
 Best Local Similarity 31.9%; Pred. No. 34;
 Matches 22; Conservative 14; Mismatches 18; Indels 15; Gaps 6;
 QY 16 PSIEHAKHTSLSSMKHDQDA-NVS--NMTFSNGKLRKGIYRNADCSHRTSAGL 72
 Db 772 PNPSE-----TLQMKKDNITAHNISRLTVSECK-KLGVLSA--CGHH-----GP 819
 QY 73 TLQDLQMC 81
 Db 820 YIPDLVFWC 828
 RESULT 13
 Q9X2G7 PRELIMINARY: PRT: 296 AA.
 ID Q9X2G7
 AC Q9X2G7: 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Hypothetical protein TM1852.
 GN TM1852.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OC NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=MSB8 / DSM 3109;
 RC MEDLINE=99287316; PubMed=10360571;
 RC Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RC Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RC McDonald L., Utterback T.R., Malek J.A., Liner K.D., Garrett M.M.,
 RC Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RC Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RC Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima."
 RT Nature 399:323-329(1999).
 RL EMBL: AE001822; AAD36914.1;
 RL TIGR: TM1852;
 DR Hypothetical protein: Complete proteome.
 DR Hypothetical protein: Complete proteome.
 SO SEQUENCE 296 AA; 34197 MW; 1183960CA5C3D2C6 CRC64;

Query Match 14.7%; Score 67; DB 16; Length 296;
 Best Local Similarity 27.3%; Pred. No. 7.4; 19; Indels 10; Gaps 3;
 Matches 15; Conservative 11; Mismatches 19
 QY 33 DQD---ANVSMFTSNGKLRKYG---IYRNADCSHRTSAGLTLQDLQMC 81
 Db 244 EEDMEKFGVPPVNFSDAMIEYNGYVYGAADNC---TALATPVEKMKWC 294

RESULT 14
 Q9FT49 PRELIMINARY: PRT: 307 AA.
 ID Q9FT49
 AC Q9FT49: 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE Hypothetical 34.9 kDa protein.
 GN T25B15.100.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Rudé S.,
 RA Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.;
 RA Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 RL (2)
 RP SEQUENCE FROM N.A.
 RP EV Arabidopsis sequencing project;
 RA Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AL132972; CAC07924.1;
 DR Hypothetical protein.
 DR SEQUENCE 307 AA; 34863 MW; DC8746CB47D8F92E CRC64;
 Query Match 14.7%; Score 67; DB 10; Length 307;
 Best Local Similarity 18.3%; Pred. No. 7.8; 26; Indels 22; Gaps 2;
 Matches 15; Conservative 19; Mismatches 18
 QY 20 HEAKHTSLSSMKHDQDA-NVS--NMTFSNGKLRKGIYRNADCSHRTSAGL 72
 Db 149 HDEYKVLSEFWHMKRSEHIVLGAFTSWKTKQCHIHLPYSQG--ITINGVLYIG 207
 QY 59 ADICSHRYTSAGLTLQDLQMC 80
 Db 208 AMTDDKCVLMSFDLTSBDVGVW 229
 RESULT 15
 Q71146 PRELIMINARY: PRT: 478 AA.
 ID Q71146
 AC Q71146: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE Envelope glycoprotein gp120 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=VE2;
 RC MEDLINE=96093896; PubMed=7576917;
 RC Quinones-Water M.E., Dopazo J., Este J.A., Rota T.R., Domingo E.;
 RA "Molecular characterization of human immunodeficiency virus type 1
 RA isolates from Venezuela."
 RT Aids Res. Hum. Retroviruses 11:605-616(1995).
 RL Aids Res. Hum. Retroviruses 11:605-616(1995).
 RP SEQUENCE FROM N.A.
 RP STRAIN=VE2;
 SO SEQUENCE 478 AA; 50000 MW; 1183960CA5C3D2C6 CRC64;

Search completed: December 8, 2002, 19:33:32
Job time : 68.2516 secs

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OM protein - protein search, using sw model
Run on: December 8, 2002, 17:26:33 ; Search time 41.2387 Seconds
(without alignments)
219.722 Million cell updates/sec

Title: US-09-880-457-4_COPY-20_87
Perfect score: 373
Sequence: 1 HEAHTSLSSMKHDDMANV.....TSAGLTLDLQWCMRIH 68
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358	96.0	95	23	AAU83632
2	178	47.7	152	22	AAU67248
3	178	47.7	150	21	AAU83632
4	178	47.7	244	23	AAU86148
5	178	47.7	244	23	AAU78286
6	178	47.7	246	19	AAU83020
7	178	47.7	317	19	AAU83195
8	178	47.7	317	19	AAU83018
9	178	47.7	317	19	AAU69957
10	178	47.7	317	19	AAU68293

11	178	47.7	317	21	AAU84417	Amino acid sequenc
12	178	47.7	317	22	AAU87238	Human receptor act
13	178	47.7	317	22	AAU04426	Human receptor act
14	178	47.7	317	22	AAU01993	Human full-length
15	178	47.7	317	23	AAU80134	Human RANKL polype
16	178	47.7	317	23	AAU78285	Human TRANCE prote
17	178	47.7	170	22	AAU08386	Mouse FLAG-murine
18	175	46.9	318	22	AAU82092	Rat osteoclast dif
19	174	46.6	245	20	AAU71873	Human TRANCE Hom
20	172	46.1	139	21	AAU91023	Mouse OBM protein
21	172	46.1	160	21	AAU80272	Amino acid sequenc
22	172	46.1	173	21	AAU84421	Amino acid sequenc
23	172	46.1	173	21	AAU84425	DNA encoding osteo
24	172	46.1	187	21	AAU84424	An osteoprotegerin
25	172	46.1	188	21	AAU84420	Amino acid sequenc
26	172	46.1	188	21	AAU84423	An osteoprotegerin
27	172	46.1	198	19	AAU83019	A murine OCIF-bind
28	172	46.1	244	19	AAU69956	NF-KB receptor act
29	172	46.1	294	19	AAU68282	Murine receptor ac
30	172	46.1	294	22	AAU04425	Murine receptor ac
31	172	46.1	294	22	AAU04425	Murine RANKL (rece
32	172	46.1	294	22	AAU04425	Human osteoprotege
33	172	46.1	316	19	AAU83017	Osteoclastogenesis
34	172	46.1	316	19	AAU83017	Amino acid sequenc
35	172	46.1	316	19	AAU83017	Amino acid sequenc
36	172	46.1	316	21	AAU84418	Murine TRANCE. Mu
37	172	46.1	316	21	AAU84418	Mouse OBM protein
38	172	46.1	316	21	AAU84418	Amino acid sequenc
39	172	46.1	316	23	AAU78289	Mouse TRANCE prote
40	172	46.1	316	23	AAU78289	GlutathioneStransf
41	172	46.1	409	23	AAU7115	Murine GST-modf tu
42	172	46.1	409	23	AAU7115	Amino acid sequenc
43	172	46.1	501	22	AAU84420	A murine osteoprot
44	172	46.1	173	21	AAU84422	An osteoprotegerin
45	145	38.9	173	21	AAU84426	

ALIGNMENTS

RESULT 1	AAU83632 standard; Protein; 95 AA.
ID	AAU83632
XX	AAU83632: (first entry)
AC	08-MAY-2002
DT	Human PRO protein, Seq ID No 82.
DE	Human: secreted protein; PRO; tumour; lung cancer; colon cancer;
XX	breast cancer; prostate tumour; rectal tumour; liver tumour;
KW	pericyte cell proliferation; chondrocyte cell proliferation;
KW	tumour necrosis factor-alpha.
XX	
OS	Homo sapiens.
XX	
PN	WO200208288-A2.
XX	
PD	31-JAN-2002.
XX	
PF	29-JUN-2001; 2001WO-US21066.
XX	
PR	20-JUL-2000; 2000US-219556P.
PR	25-JUL-2000; 2000US-220385P.
PR	25-JUL-2000; 2000US-220607P.
PR	25-JUL-2000; 2000US-220607P.
PR	25-JUL-2000; 2000US-220624P.
PR	25-JUL-2000; 2000US-220638P.
PR	25-JUL-2000; 2000US-220644P.
PR	25-JUL-2000; 2000US-220666P.
PR	25-JUL-2000; 2000US-220893P.
PR	26-JUL-2000; 2000US-220893P.
PR	28-JUL-2000; 2000WO-US20710.

PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX

(GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Garney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX WPI: 2002-172001/22.
 DR N-PSDB; ABR33576.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT tumour or liver tumour -
 XX
 XX Claim 11; Figure 82; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor- α from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.

XX Sequence 95 AA;

Query Match
 Best Local Similarity 96.0%; Score 358; DB 23; Length 95;
 Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HEAHTSLSSMKHODVANNVSMFTSNGKLRVKGITYRNADICSRHRYTSAGLTLODLOL 60
 DB 20 HEAHTSLSSMKHODVANNVSMFTSNGKLRVKGITYRNADICSRHRYTSAGLTLODLOL 60
 OY 61 WCNLRIT 67
 DB 80 WCNLRISV 86

RESULT 2

AA087248

XX AAB67248 standard; protein: 152 AA.

AC AAB67248;

DT 18-APR-2001 (first entry)

DE Human RANKL.

XX Human; Apo2 ligand: divalent metal ions; viral infection; cancer.

OS Homo sapiens.

XX

PN WO200100832-A1.

XX 04-JAN-2001.

PD 26-JUN-2000; 2000WO-US17579.

XX 28-JUN-1999; 99US-0141342.

PR (GETH) GENENTECH INC.

XX Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;
 PI O'Connell M, Pai R, Shahrokh Z, Simmons L;
 XX WPI: 2001-123012/13.

XX Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications -
 XX Disclosure; Fig 3; 60pp; English.

XX The present invention relates to a formulation comprising Apo-2
 CC ligand and divalent metal ions. Apo-2 ligand and the formulation
 CC of divalent metal ions for treating cancers and viral infections. Addition
 CC containing Apo-2 ligand results in increased yield and stability
 CC of Apo-2 ligand trimers.

XX Sequence 152 AA;

Query Match
 Best Local Similarity 47.7%; Score 178; DB 22; Length 152;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHTSTSSMKHODVANNVSMFTSNGKLRVKGITYRNADICSRHRYTSAGLTLODLOL 60
 DB 17 SHRVSLSSMKHODVANNVSMFTSNGKLRVKGITYRNADICSRHRYTSAGLTLODLOL 76

RESULT 3

XX AAB08273 standard; protein: 160 AA.

AC AAB08273;

DT 04-DEC-2000 (first entry)

DE Amino acid sequence of a human TNF ligand QPGL.

XX ACP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;

KW type II transmembrane protein; B cell stimulatory factor;

KW inflammatory disorder; immune disorder; rheumatoid arthritis;

XX lupus and graft versus host disease.

OS Homo sapiens.

XX WO200047740-A2.

PN 17-AUG-2000.

PD 11-FEB-2000; 2000WO-US03653.

XX 12-FEB-1999; 99US-0119906.

PR 18-NOV-1999; 99US-0166271.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Hsu H;

PI WPI: 2000-558217/51.

DR Novel polypeptides comprising tumour necrosis factor ligand family

PT proteins, useful for treating inflammatory and immune disorders, e.g.

XX

XX The present invention relates to a new method of treating a mammal
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth. The method of the invention involves administering to
 CC the mammal a tumour necrosis factor-related activation induced cytokine
 CC (TRANCE)-modulating agent. The method is useful for treating a cytokine
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth, where the disorder comprising insufficient cartilage or
 CC craniofacial growth is selected from dwarfism, osteopetrosis,
 CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
 CC arthritis, and disorders comprising excessive cartilage or skeletal
 CC growth are selected from acromegaly, gigantism, exostosis, cartilage
 CC exostosis, bursecta and multiple osteochondrocyte exostoses. The method
 CC is useful for inhibiting chondrocyte differentiation. The present amino
 CC acid sequence represents the human TRANCE protein, splice variant 2, of
 CC the invention. TRANCE is a member of the tumour necrosis factor family
 CC and acts directly on cartilage-producing cells (chondrocytes).
 SO Sequence 244 AA;

Query Match 47.7%; Score 178; DB 23; Length 244;
 Best Local Similarity 60.0%; Pred. No. 4.1e-15;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHDQMANVSNMTFSGKLRVK--GIYRNADICSRHRYVSAGLTLDL 60
 Db 106 SHKYSLSWYHDQMAKISNMTFSGKLIYNQDGFYLVANICFRHHTSGDLATEYLDL 165

RESULT 6
 AAW83020
 ID AAW83020 standard; Protein: 246 AA.

AC AAW83020;
 XX 10-FEB-1999 (first entry)

DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).

KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KM Osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 OS human.

XX Homo sapiens.
 XX
 PN WO9846644-A1.

XX 22-OCT-1998.
 PD
 XX

PF 15-APR-1998; 98WO-JP01728.

PR 02-DEC-1997; 97JP-0332241.

PR 15-APR-1997; 97JP-0097808.

PR 09-JUN-1997; 97JP-0151434.

PR 12-AUG-1997; 97JP-0217897.

PR 21-AUG-1997; 97JP-0224803.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morioka T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;

DR WPI: 1998-594563/50.
 DR N-PSDB: AAV69899.

XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism

XX Example 28; Pages 119-120; 151pp; Japanese.

CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone.
 CC Absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC formation factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modulators of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC components of drugs.
 SO Sequence 246 AA;

Query Match 47.7%; Score 178; DB 19; Length 246;
 Best Local Similarity 60.0%; Pred. No. 4.2e-15;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

OY 3 AHKTSLSMKHDQMANVSNMTFSGKLRVK--GIYRNADICSRHRYVSAGLTLDL 60
 Db 108 SHKYSLSWYHDQMAKISNMTFSGKLIYNQDGFYLVANICFRHHTSGDLATEYLDL 167

RESULT 7
 AAW83195
 ID AAW83195 standard; Protein: 317 AA.

AC AAW83195;
 XX 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the pcDNA/hnopbpl.1insert.

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
 KM osteoporosis; osteoclast maturation; bone disease; metastasis; ODAK;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 OS Paget's disease.

XX Homo sapiens.
 XX
 PN WO9846751-A1.

XX 22-OCT-1998.
 PD
 XX

PF 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

PA (AMGE-) AMGEN INC.

XX Boyle WJ;

PI WPI: 1998-594578/50.
 DR N-PSDB: AAV70285.

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis

XX Claim 19; Fig 4; 47pp; English.

XX The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for

CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODMR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences; also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.

CC Sequence 317 AA:

Query Match 47.7%; Score 178; DB 19; Length 317;
 Best Local Similarity 60.0%; Pred. No. 5.8e-15;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 3 AHKTSLSWKHODMANVSNMFTSNGKLRVK--GIYYRNADICSRHRYTSAGITLQDL 60
 :||| ||||| ||: ||: ||||| ||||| ||: ||: ||||| ||: ||: |||||
 Db 179 SHKVSLSWYHDSGMWAKISNMFTSNGKLIYNQDGFYLYANICFRHHTSGDLATEYQL 238

RESULT 8
 AAM83018 standard; Protein; 317 AA.

AC AAM83018;

DT 10-FEB-1999 (first entry)

DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).

XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;

KM Osteoclast; bone absorption factor; bone disorder; calcium metabolism;

KW human.

XX Homo sapiens.

OS Homo sapiens.

PN WO9846644-A1.

XX 22-OCT-1998.

PD 15-APR-1998; 98WO-JP01728.

XX 02-DEC-1997; 97JP-0332241.

PR 15-APR-1997; 97JP-0097808.

PR 09-JUN-1997; 97JP-0151434.

PR 12-AUG-1997; 97JP-0217897.

PR 21-AUG-1997; 97JP-0224803.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

PA Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;

PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;

PI Washida N, Yamaguchi K, Iano K, Yasuda H;

XX WPI: 1998-594563/50.

DR N-PSDB; AAV69887.

XX Protein binding to osteoclastogenesis inhibitory factor - useful

PT for, e.g. treatment and investigation of disorders of bone and

XX calcium metabolism

Claim 36; Pages 113-114; 151pp; Japanese.

XX The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins

CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (OBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.

CC Sequence 317 AA:

Query Match 47.7%; Score 178; DB 19; Length 317;
 Best Local Similarity 60.0%; Pred. No. 5.8e-15;
 Matches 36; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 3 AHKTSLSWKHODMANVSNMFTSNGKLRVK--GIYYRNADICSRHRYTSAGITLQDL 60
 :||| ||||| ||: ||: ||||| ||||| ||: ||: ||||| ||: ||: |||||
 Db 179 SHKVSLSWYHDSGMWAKISNMFTSNGKLIYNQDGFYLYANICFRHHTSGDLATEYQL 238

RESULT 9
 AAM69957 standard; Protein; 317 AA.

AC AAM69957;

DT 08-OCT-1998 (first entry)

DE NF-kB receptor activator RANK ligand (RANKL).

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis;

KW RANKL; RANK ligand; tumour necrosis factor; TNF.

OS Homo sapiens.

XX WO9828426-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23775.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

XX (IMMEX) IMMEX CORP.

PA Anderson DM, Galibert LJ, Maraskovsky E;

PI WPI: 1998-377657/32.

DR N-PSDB; AAV41378.

XX New isolated ligand for receptor activator of NF-kappa B - used to

XX develop products for augmenting an immune response for inhibiting an

XX inflammatory response and for protection of cells

XX Claim 27; Pages 59-60; 80pp; English.

XX This represents a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease

transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or of the presence or distribution of RANK transcripts. The present sequence is RANK ligand (RANKL) protein from human.

Sequence 317 AA:

Query Match	Best Local	Similarity	Score	178;	DB	22;	Length	317;	
Matches 36;	Conservative	5;	Mismatches	17;	Indels	2;	Gaps	1;	
3	AHKTSLSSMKHDDQWAVNSMNFPSNCKLRVK--GIYYRNADICSRHRVTSAGLTLDLQ	60	60.0%	5;	17;	Indels	2;	Gaps	1;
179	SHKYSLSWHDYRDGMARISNMTFSNGKLITVNOGFFYLVANICFRHHTSGDILATETIQL	238							

RESULT 13

AAE04426

AAE04426 standard; Protein: 317 AA.

AAE04426;

04-SEP-2001 (first entry)

Human receptor activator of NF- κ B ligand (huRANKL) protein.

Human receptor activator of NF- κ B; RANK; tumour necrosis factor; TNF

Human; receptor activator of NF- κ B; RANK; ligand; immune response; CD40; TNF receptor-associated factor; TRAF; ligand; transmembrane protein.

chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.

Homo sapiens.

Key	Location/Qualifiers
Region	162..317
	/note="Receptor binding region"

US6242213-B1.

05-JUN-2001.

22-DEC-1997; 97US-0995659.

23-DEC-1996; 96US-0059978.

07-MAR-1997; 97US-0077181.

14-OCT-1997; 97US-0064671.

(IMMV) IMMUNEX CORP.

Anderson DM;

WPI: 2001-407216/43.

N-PSDB: AAMD08715.

New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF- κ B receptor activator) of the receptor activator of NF- κ B (RANK) -

Claim 1: Column 65-66; 43pp: English.

The present invention relates to receptor activator of NF- κ B (RANK) to DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular

CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC present amino acid sequence is full-length human RANL1 (huRANL1)
CC protein. The RANL1 gene is located in chromosome 13q14.
XX
XX

Query Match	47.7%	Score 178;	DB 22;	Length 317.
Best Local Similarity	60.0%			

Conservative	Mismatches	Indels	Gaps
36	5	17	2

3 AKHLSLSMKHDQDMANVSNMTFSNGKLRV -GIYRMADICSRRHVTSGAGLLDQL 60
179 SHKYSLSMTWHDRCWAKISNMTFSNGKLIYNQDGFYLYANICFRHHSTSGTAVRQ 120

RESULT	15
ABB08134	
ID	ABB08134
standard:	protein: 317

10-SEP-2000

Human RANKL polypeptide.

W0200236141-A2.

10-MAY-2002.

30-OCT-2001;

02-NOV-2000; 2000US-245721P.

(IMMV) IMMUNEX CORP.

Lynch DH, De Smedt TR
Thomas FK.

DATE: 11/11/2003
BY: J. MILLER
WPI: 3003.F0011

WMA, 2002-300114/53.

treating an individual
chickenpox or AIDS,

antigen-specific T cells, T cell enhancing factor, and interleukin-2, administered as a combination of dendritic cell mobilization factor or maturation agent, T cell enhancing factor, and interleukin-2.

Disclosure; Page 42-43; 43pp; English.

The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism. The method involves administering a pathogenic or opportunistic organism. The method agent: (a) dendritic cell mobilization factor; (b) dendritic cell maturation agent; (c) dendritic cell activation factor; (d) T cell enhancing factor; (e) activated, antigen-specific T cells. The methods are useful for treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria (e.g. *M. tuberculosis*), yeast, fungi (e.g. *C. albicans*) or protozoa (e.g. *T. cruzi*), which causes Chagas' disease). The antibodies are especially useful for treating an individual suffering from immunosuppression by enhancing a lymphocyte-mediated immune response. In particular, the method is useful for treating inflammation, chickenpox, oral or genital herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis AIDS, T cell leukemia or T cell lymphoma. The activated antigen-presenting dendritic cells are useful as a vaccine adjuvant. The present sequence represents a human RANKL polypeptide fragment.

1
2
3
4

GenCore version 5.1.3
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OM protein - protein search, using sw model
December 8, 2002, 17:28:38 ; Search time 16.2774 Seconds
(without alignments)
Run on: 221.684 Million cell updates/sec

Title: US-09-880-457-4
perfect score: 455
Sequence: 1 MATLTLSDLLILLIRISH.....TSAGILDLQMLCNLRTH 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	180.5	39.7	317	1	TN1L_HUMAN
2	177.5	39.0	318	1	TN1L_RAT
3	176	38.7	316	1	TN1L_MOUSE
4	78.5	17.3	501	1	CS02_DROME
5	66	14.5	310	1	SC65_YARLI
6	65.5	14.4	641	1	NUSM_ALUMA
7	64	14.3	251	1	Y108_CHLTR
8	63.5	14.1	334	1	GUB_CLOTM
9	63.5	14.0	263	1	PYR PICAN
10	63	13.8	119	1	IL1B_HAEIN
11	61.5	13.5	269	1	IL1B_HRIIV
12	61.5	13.5	329	1	IPNS_STRCL
13	61.5	13.5	1078	1	IPNS_BOVIN
14	61	13.4	851	1	NUD1_YEAST
15	61	13.4	2144	1	GLT1_YEAST
16	60.5	13.3	1451	1	SPT6_YEAST
17	60	13.2	301	1	TRAP_ECOLI
18	60	13.2	301	1	Y186_MYCPN
19	59.5	13.1	783	1	AP22_SULSO
20	59.5	13.1	216	1	SCAH_ECOLI
21	59.5	13.1	329	1	IPNS_STRCL
22	59.5	13.0	561	1	ATKA_ANAST
23	58.5	12.9	958	1	AMYG_DEBOC
24	58.5	12.9	1859	1	GBFL_HUMAN
25	58.5	12.9	551	1	FIXN_AZOC
26	58	12.7	478	1	DISR_AGRH
27	57.5	12.6	525	1	APPL_YEAST
28	57.5	12.6	525	1	GSNC_PEA
29	57.5	12.6	677	1	RN14_YEAST
30	57.5	12.6	1856	1	GBFL_CRIGR
31	57.5	12.6	2156	1	RPL_HUMAN
32	57.5	12.6	72	1	COR2_DROME
33	57	12.5	1	1	COR2_DROME

34	57	12.5	720	1	KRE6_YEAST
35	57	12.5	1444	1	KRE6_YEAST
36	57	12.5	1585	1	P3K3_DICDI
37	56.5	12.4	158	1	2SS_SOYBN
38	56.5	12.4	161	1	VP7_BPPH6
39	56.5	12.4	286	1	TEHB_HAEIN
40	56.5	12.4	333	1	IPNS_STRCL
41	56.5	12.4	404	1	FCGL_MOUSE
42	56.5	12.4	404	1	ISCS_METTE
43	56.5	12.4	544	1	ISCS_METTE
44	56.5	12.4	550	1	YSR1_CAEEL
45	56.5	12.4	587	1	ULB4_HCMVT

ALIGNMENTS

RESULT 1
ID TN1L_HUMAN STANDARD: PRT: 317 AA.
AC 014788: 014723: Q9P203: Q96Q17;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast DE induced cytokine factor) (ODF).
DE TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID:9606;
OX [1]
RN .SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Bone marrow, and Peripheral blood;
RC MEDLINE=98032977; PubMed=9367155;
RX Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Gallbert L.;
RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function";
RT Nature 390:175-179(1997).
RL [2]
RN .SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Lymph node;
RC MEDLINE=98227661; PubMed=9568710;
RX Tacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Xian Y.-X., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Sullivan J., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;
RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation";
RT Cell 93:165-176(1998).
RL [3]
RN .SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RP Ikeda T., Kuroyama H., Hirokawa K.;
RA "Determination of human RANKL isoforms";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RN .SEQUENCE OF 73-317 FROM N.A.
RP TISSUE=Thymocytes;
RC MEDLINE=97460112; PubMed=9312132;
RX Wong B.R., Rho J., Aron J., Robinson E., Orlick J., Chao M., Lee S.Y., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;
RA "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells";
RT J. Biol. Chem. 272:25190-25194(1997).
RL [5]
RN .SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=Tongue;

RX MEDLINE-20175237; PubMed-10708588;
 RA Nagai M., Kyumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RL encoding a secreted form of ODF/TNFRANK that induces osteoclast
 formation.";
 CC Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Promotes the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/SODF and 3;
 CC are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
 CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
 CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
 CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF019047; AAB86811.1; -
 DR EMBL: AF05312; AAC39731.1; -
 DR EMBL: AB064269; BAB79694.1; -
 DR EMBL: AB061227; BAB71768.1; -
 DR EMBL: AB064270; BAB79695.1; -
 DR EMBL: AF013171; AAC51762.1; -
 DR HSSP: AB037599; BAA90488.1; -
 DR HSSP: P50591; IDOG. -
 DR Gene: HGNC:11926; TNFSF11.
 DR MIM: 602642; -
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; FALSE_NEG.
 DR PROSITE: PS00049; TNF_2; 1.
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 KW Signal anchor; Alternative splicing.
 FT CHAIN 1 317
 FT DOMAIN 140 317
 FT TRANSMEM 48 68
 FT DOMAIN 69 317
 FT SITE 139 140
 FT CARBOHYD 171 171
 FT CARBOHYD 198 198
 FT VARSPIC 1 47
 FT CONFLICT 1 73
 FT CONFLICT 194 194
 FT SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;
 Query Match 39.7%; Score 180.5; DB 1; Length 317;

Best Local Similarity 59.7%; Pred. No. 1.3e-13;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 OY 15 IPSTSHAKHTSISNKHDDMANVSNMTFSNGKLVK--GIYRNADICSHRTYSAGL 72
 DB 175 IPGSGS---HKVSLSSWYHDKRMKISMFTSNCKLIVNDGRIYLYANICFRHHTSGDL 231
 OY 73 TLQDLQ 79
 DB 232 ATREYIQL 238
 RESULT 2
 ID TN11_RAT STANDARD; PRT; 318 AA.
 AC Q9SESE2; Q91219;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
 DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
 DE induced cytokine) (TNF) (osteoprotegerin ligand) (OPGL) (osteoclast
 DE TNFSF11 OR RANKL OR TNF) (ODE).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TxId=10116;
 RP [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Tibial bone;
 RA MEDLINE=20540945; PubMed=11092398;
 RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
 RA Zheng M.H.;
 RT "Cloning, sequence and functional characterization of the rat
 RL homologue of receptor activator of NF-kB ligand.";
 RN J. Bone Miner. Res. 15:2178-2186(2000).
 RP [2]
 RC SEQUENCE OF 266-318 FROM N.A.
 RC STRAIN=Fischer 344;
 RA Olgren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savvas A.,
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,
 RA Marks S.C. Jr.;
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
 RL the TNFSF11 (TNF, RANKL, ODF, OPGL) gene.";
 RT Int. J. Dev. Biol. 45:853-859(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Promotes the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF187319; AAG17031.1; -
 DR EMBL: AF425669; AAL23963.1; -

CC -1- SUBUNIT: Homotrimer.
 CC (isoform 1 and 2): Cytoplasmic (isoform 3).
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
 CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
 CC TRABECULAR BONE AND LUNG.
 CC -1- PTM: N-glycosylated.
 CC by proteolytic processing. The cleavage may be catalyzed by
 CC ADAM17. A further shorter soluble form was observed.
 CC -1- DISEASE: DEFICIENCY IN TNFSF1 RESULTS IN FAILURE TO FORM LOBULO-
 CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
 CC OF NEONORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS, WITH
 CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
 CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
 CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
 CC HYPERTROPHIC CHONDROCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC EMBL: AF03170; AAC71061.1; -
 CC DR EMBL: AF019048; AAB66812.1; -
 CC DR EMBL: AF037173; AAC40113.1; -
 CC DR EMBL: AB008426; BAA25425.1; -
 CC DR EMBL: AB020439; BAA36970.1; -
 CC DR EMBL: AB022037; BAA36970.1; JOINED.
 CC DR EMBL: AB022038; BAA36970.1; JOINED.
 CC DR EMBL: AB032773; BAA97257.1; -
 CC DR EMBL: AB032773; BAA97257.1; -
 CC DR EMBL: AB032773; BAA97257.1; -
 CC DR PDB: 1J72; 12-SEP-01.
 CC DR PDB: 1J72; 12-SEP-01.
 CC DR MGD: MGI:1100089; Tnfsl1.
 CC DR InterPro: IPR003636; TNF_abc.
 CC DR Pfam: PF00229; TNF_1.
 CC DR SMART: SM00207; TNF_1.
 CC DR PROSITE: PS00251; TNF_1; FALSE_NEG.
 CC DR PROSITE: PS0049; TNF_2; 1.
 CC KW CytoKine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 CC Signal-anchor, 3D-structure; Alternative splicing.
 CC CHAIN 1 316
 CC DOMAIN 139 316
 CC TRANSMEM 49 69
 CC DOMAIN 70 316
 CC SITE 138 316
 CC CARBOHYD 197 197
 CC VARSPLIC 262 262
 CC VARSPLIC 1 117
 CC VARSPLIC 14 44
 CC CONFLICT 99 99
 CC CONFLICT 141 143
 CC SEQUENCE 316 AA; 34944 MW; 08DF6A2BE00967A CMC64;
 CC Query Match
 CC Best Local Similarity 38.7%; DB 1; Length 316;
 CC 55.48; Pred. No. 4.4e-13;

Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;
 QY 17 SISFAHRTSISKKHODANVSNMTFSNGKLRK--GIYNNADICSRHRTSAGLTL 74
 Db 173 SIPGSKHVTLSWYHIDRGWAKISNMTLSNGKLRKADQFVYLVANICRHETSGSPT 232
 QY 75 QDIQL 79
 Db 233 DYIQL 237
 RESULT 4
 CSD2_DROME
 ID CSD2_DROME STANDARD; PRT; 501 AA.
 AC Q9VMT6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DE 16-OCT-2001 (Rel. 40, Last sequence update)
 GN Probable cytochrome P450 28d2 (EC 1.14.14.1) (CYP28D2)
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champ M., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Bailes R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fostler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Fleischmann W.,
 RA Glodex C., Gabriellian A.E., Garg N.S., Gelbart W.M., Fleischmann W.,
 RA Harris N.L., Harvey D., Heiman T.J., Gu Z., Guan P., Harris M.,
 RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
 RA Jalali M., Kalush F., Karpman G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shne B.C., Sheng-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Spradling A.C., Stappleton M., Strong R., Sun E.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodard D., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RP CONCEPTUAL TRANSLATION.
 RA Nelson B.;
 CC Unpublished observations (SEP-2000).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE METABOLISM OF INSECT HORMONES AND
 CC IN THE BREAKDOWN OF SYNTHETIC INSECTICIDES (BY SIMILARITY).


```

CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC (potential).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous
CC gene model prediction.
-----
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-----
CC EMBL: AE003609; AAF52225.1; ALT_SEQ.
CC FlyBase: FBgn0031688; CYP28d2.
CC InterPro: IPR001128; Cytochrome_P450.
CC Pfam: PF00067; P450.1.
CC PRINTS: PR00385; CYTOCHROME_P450.1.
CC PROSITE: PS00086; Cytochrome P450.
CC Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
CC Endoplasmic reticulum; Hypothetical protein.
CC BINDING 446 446 HEME (BI SIMILARITY).
CC SEQUENCE 501 AA; 58222 MW; 9AD85F249390A655 CRC64;
SQ
Query Match 17.3%; Score 78.5; DB 1; Length 501;
Best Local Similarity 20.0%; Pred. No. 0.15;
Matches 24; Conservative 17; Mismatches 44; Indels 35; Gaps 4;
QY 1 MAILTSLDILLLPSISHEAKTSLSSWKHDQDMANVSNMTFSGKRL----- 49
DB 74 VGFETTRVQLTWCEYIHKIYATFRSP-HNNEKRNVNKKTDMLGNPFVLTDGEW 132
OY 50 -----RVKGIYRNADICSR-----HRVTSAGLTLDIOLMCLRTII 86
DB 133 KERSEIMPALSPRVKAVPVSGSVCKRFVEYIRROOMATSEGDAMLSICTTTEV 192
RESULT 5
SC65_YARLI STANDARD; PRT; 310 AA.
AC P41922;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Signal recognition particle SC65 subunit.
DE SEC65 OR SRP19.
GN Yarrowia lipolytica (Candida lipolytica).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RT (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 20460 / W29;
RC MEDLINE=98085978; PubMed=9426009;
RA Sanchez M., Beckerich J.M., Galliardin C., Dominguez A.;
RA "Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a
RA component of the yeast signal recognition particle displaying
RA homology with the human SRP19 gene."
RT Gene 203:75-84(1997).
CC -1- FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE
CC IN TARGETING SECRETORY PROTEINS TO THE ROUGH ENDOPLASMIC RETICULUM
CC MEMBRANE. IT MUST BE INVOLVED INTIMATELY IN THE TRANSLLOCATION OF A
CC WIDE VARIETY OF PROTEIN SUBSTRATES (BY SIMILARITY).
CC -1- SUBUNIT: FUNGAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA
CC MOLECULE (SCR1) AND AT LEAST SEVEN PROTEIN SUBUNITS: SRP72, SRP68,
CC SRP54, SEC65, SRP21, SRP14 AND SRP7 (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SRP19 FAMILY.
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-----
CC EMBL: Z22570; CA86293.1;
CC InterPro: IPR002778; SRP19.
CC Pfam: PF01922; SRP19.1.
CC ProDom: PD006609; SRP19; 1.
CC Signal recognition particle; RNA-binding; Ribonucleoprotein.
CC SEQUENCE 310 AA; 35487 MW; D65EC9F0C80114C3 CRC64;
SQ
Query Match 14.5%; Score 66; DB 1; Length 310;
Best Local Similarity 41.5%; Pred. No. 2.4;
Matches 17; Conservative 17; Mismatches 3; Indels 14; Gaps 3;
QY 12 LLLPSISHEAKTSLSSWKHDQDMANVSNMTFSGKRLRVK 52
DB 161 MLTLPST-YEAHKT-----HPRDWMAN-----PGRVAVQ 187
RESULT 6
NUSM_ALIMA STANDARD; PRT; 641 AA.
AC P50365;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3).
DE NDS OR NAD5.
GN Allomyces macrogynus.
OS Allomyces macrogynus.
OC Eukaryota; Fungi; Chytridiomycota; Blastocladiiales; Blastocladiaceae;
OC Allomyces.
OX NCBI_TaxID=28583;
RT (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 46923 / BURMA 3-35 (350C);
RC PAQUIN B., Roewer I., Wang Z., Lang B.F.;
RA "A robust fungal phylogeny using the mitochondrially encoded nads
RA protein sequence."
RT Can. J. Bot. 73:5180-5185(1995).
RT [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 46923 / BURMA 3-35 (350C);
RC MEDLINE=96226032; PubMed=8636971;
RA Paquin B., Lang B.F.;
RA "The mitochondrial DNA of Allomyces macrogynus: the complete genomic
RA sequence from an ancestral fungus."
RT J. Mol. Biol. 255:688-701(1996).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-----
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-----
CC EMBL: U17010; AAB05846.1;
CC EMBL: U41288; AAC49228.1;
CC InterPro: IPR003916; NADH_oxred5.
CC InterPro: IPR001750; Oxidored_g1.
CC InterPro: IPR001516; Oxidored_g1_N.
CC Pfam: PF00361; oxidored_g1_N.1.
CC Pfam: PF00662; oxidored_g1_N.1.
CC PRINTS: PR01434; NADHGNAS5.
CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
CC SEQUENCE 641 AA; 70674 MW; 9C64C376B72E7E61 CRC64;
SQ
Query Match 14.4%; Score 65.5; DB 1; Length 641;

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Best Local Similarity 27.9%; Pred. No. 6.5;
Matches 19; Conservative 12; Mismatches 28; Indels 9; Gaps 2;

OY 2 AITLTLISGLILIPISISHEAK-----TSLSSWKHDODW--ANVSMTFSNCKLAVK 52
DB 522 SLGLISLIVLKDKPKKHSIKPEGLINTVITFWLSSKSYWFDVNTYVLISSGLHFG 581
OY 53 GIVYRNAD 60
DB 582 GIVARDID 589

RESULT 7
Y108_CHLTR
ID Y108_CHLTR STANDARD; PRT; 251 AA.
AC 084110;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein CT108.
GN CT108.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/TW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.
CC CC
CC CC
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CC or send an email to license@sib-sib.ch).
CC CC
CC EMBL: AE001284; AAC67699.1;
CC DR PHC1-2DPAC: 084110;
CC DR InterPro: IPR002678; DUF34.
CC DR Pfam: PF01784; DUF34; 1.
CC DR TIGRFAMs: TIGR00486; DUF34; 1.
CC KW Complete proteome.
CC SQ SEQUENCE 251 AA; 27474 MW; AAC2F6BE7517298E CRC64;

Query Match 14.3%; Score 65; DB 1; Length 251;
Best Local Similarity 26.4%; Pred. No. 2.5;
Matches 23; Conservative 13; Mismatches 27; Indels 24; Gaps 4;

OY 7 SLQILILIPISISHEAKTSLSSWK--HDDKMANVSMNTFSNCKLRYKGI-----54
DB 91 NIQILAVHLP---DAHTTIGNMKKAYARDIGWQLSFFGSPSLGKGVFPEMEVHDFI 147
OY 55 -----YRNADIC--SRHRTVTSAGI 72
DB 148 SOLSAVYQTPVILAKALGKRRVSSAL 174

RESULT 8
GUB_CLOTM
ID GUB_CLOTM STANDARD; PRT; 334 AA.
AC P29716; P37074;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)

(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase) (Laminarinase).
GN LICH OR LAM1.
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27405 / DSM 1237;
RX MEDLINE=92155194; PubMed=1740123;
RA Schilling S., Schwarz W.H., Staendebauer W.L.;
RT "Structure of the Clostridium thermocellum gene licB and the encoded
RT beta-1,3-1,4-glucanase. A catalytic region homologous to Bacillus
RT lichenases joined to the reiterated domain of clostridial
RT cellulases."
RL Eur. J. Biochem. 204:13-19(1992).
RN [2]
RP PRELIMINARY SEQUENCE FROM N.A.
RC STRAIN-F7;
RX MEDLINE=92095946; PubMed=1755832;
RA Zverlov V.V., Laptev D.A., Tishkov V.I., Velikodvorskaja G.A.;
RT "Nucleotide sequence of the Clostridium thermocellum laminarinase
RT gene."
RL Biochem. Biophys. Res. Commun. 181:507-512(1991).
RN [3]
RP REVISIONS.
RA Zverlov V.V.;
RT Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RA Zverlov V.V., Velikodvorskaja G.A.;
RT "Cloning the Clostridium thermocellum thermostable laminarinase gene
RT in Escherichia coli; the properties of the enzyme thus produced."
RL Biochemol. Lett. 12:811-816(1990).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
CC in beta-D-glucans containing 1,3- and 1,4-bonds.
CC -1- SUBUNIT: MAY FORM PART OF A MULTIMERIC COMPLEX (CELLULOSE).
CC WELL AS IN OTHER C.THERMOCELLUM CELLULOSE ENZYMES. THIS DOMAIN
CC MAY FUNCTION AS THE BINDING LIGAND FOR THE SL COMPONENT.
CC -1- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
CC CC
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CC CC
CC EMBL: X63355; CAA44959.1;
CC DR EMBL: X58392; CAA41281.1;
CC DR PIR: S23498; S23498.
CC DR PIR: JS0611; JS0611.
CC DR HSSP: S18726; S18726.
CC DR HSSP: P23904; LAIK.
CC DR InterPro: IPR002105; Dockerin_1.
CC DR InterPro: IPR002048; EF-hand.
CC DR Pfam: PF00722; Glyco_hydro_16.
CC DR Pfam: PF00722; Glyco_hydro_16; 1.
CC DR PRINTS: PR00737; GLYHDLASE16.
CC DR PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
CC DR PROSITE: PS00018; EF_HAND_UNKNOWN_2.
CC DR PROSITE: PS00448; CLOS_CELLULOSE_RPT; 2.
CC KW Hydrolyase; Glycosylase; Signal; Repeat.
CC FT SIGNAL 1 27
CC FT CHAIN 28 334
CC FT ACT_SITE 136 136
CC FT ACT_SITE 140 140
CC FT DOMAIN 252 269
CC FT DOMAIN 273 331
CC 2 X 24 AA APPROXIMATE REPEATS.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9221044; PubMed=10206203;
RA Medlock D.N., Goh L.P., Parlane N.A., Buddle B.M.;
RT "Molecular cloning and physiological effects of brushtail possum
interleukin-beta";
RL Vet. Immunol. Immunopathol. 67:359-372(1999).
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: MONOMER.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL: AF071539; AAD21871.1; -
DR HSSP: P01584; 1HTB.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR003502; IL1_propep.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF00394; IL1_propep; 1.
DR PRINTS: PR00262; ILHBGF.
DR Prodom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
DR CycloLine: Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112 BY SIMILARITY.
FT CHAIN 1 112 INTERLEUKIN-1 BETA.
SQ SEQUENCE 269 AA; 3141 MW; 307A1FE3B627D6E7 CRC64;

Query Match 13.5%; Score 61.5; DB 1; Length 269;
Best Local Similarity 27.3%; Pred. No. 6.9;
Matches 24; Conservative 13; Mismatches 34; Indels 17; Gaps 4;

QY 12 LLLPSISHEAHTSLSS-WKHDDMANVSNNMTFS-NGKLRKGIYRNADI---CSRHR 66
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 VMVVAIEKMKHNLGLSSQFODNDLNMIFNIFQ-----EPITFNCDIYESDSFRL 122
QY 67 VTSAGLTLDLQ-----NLRTH 87
DB : : : : : : : : : : : : : : : : : : : : : :
DB 123 VSSQDCTIQDINOKCLASKASELRALH 150

RESULT 12
ID IPNS_STRCL STANDARD; PRT; 329 AA.
AC P10621:
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Isopenicillin N synthetase (EC 1.-.-.-) (IPNS) (Isopenicillin N
DE synthase).
GN PCBC.
OS Streptomyces clavuligerus.
OC Bacteria: Actinobacteria: Actinobacteria (class): Actinobacteridae:
OC Actinomycetales: Streptomycinae: Streptomycetaceae: Streptomyces.
OX NCBI_TaxID=1901;

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RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
RA Medline=88212175; PubMed=1130293;
RA Leski B.K., Aharonowitz Y., Meyerech M., Wolfe S., Vining L.C.,
RA Westlake D.W.S., Jensen S.E.;
RT "Cloning and nucleotide sequence determination of the isopenicillin N
RT synthetase gene from Streptomyces clavuligerus.";
RL Gene 62:187-196(1988).
CC -I- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS
CC FROM DELTA-L-(ALPHA-AMINODIPYL)-L-CYSTEINYL-D-VALINE (ACV) TO
CC FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
CC -I- COFACTOR: IRON AND ASCORBATE.
CC -I- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND
CC CEPHALOSPORIN.
CC -I- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC OXIDOREDUCTASES.
CC -----
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CC -----
DR EMBL: M19421; AAA26770.1; -
DR EMBL: A01132; CA000131.1; -
DR PIR: A29894; A29894.
DR HSSP: P05326; 1BLZ.
DR InterPro: IPR005123; 2OG-Ferri_Oxy.
DR InterPro: IPR002283; IPN_synth.
DR InterPro: IPR002057; Isopen_N_synth.
DR Pfam: PF03171; 2OG-Ferri_Oxy; 1.
DR PRINTS: PR00682; IPNSYNTHASE.
DR PROSITE: PS00185; IPNS_1; 1.
DR PROSITE: PS00186; IPNS_2; 1.
DR Antibiotic biosynthesis; Oxidoreductase; Iron; Vitamin C.
FT METAL 212 212 IRON (BY SIMILARITY).
FT METAL 214 214 IRON (BY SIMILARITY).
FT METAL 268 268 IRON (BY SIMILARITY).
SQ SEQUENCE 329 AA; 36958 MW; 71A1ACE9514761C CRC64;

Query Match 13.5%; Score 61.5; DB 1; Length 329;
Best Local Similarity 24.0%; Pred. No. 8.7;
Matches 18; Conservative 12; Mismatches 36; Indels 9; Gaps 2;

QY 15 IPSISHEAHTSLSSWKHD-----QDMANVSNNMTFS-NGKLRKGIYRNADICSRH 65
DB : : : : : : : : : : : : : : : : : : : : : :
DB 55 LQDVNVEFGAMTDQEKHDLAIHAVYDPNPHVNGYKAVPORKAVESFCYILNPFGEDH 114
QY 66 RYTSAGLTLDLQ-----LW 80
DB : : : : : : : : : : : : : : : : : : : : : :
DB 115 PMTAASTPMHEVNLW 129

RESULT 13
ID CYAT_BOVIN STANDARD; PRT; 1078 AA.
AC Q29450: 002856;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylyl cyclase, type VII (EC 4.6.1.1) (ATP pyrophosphate-lyase)
DE (Adenylyl cyclase).
GN ADCT7.
OS Bos taurus (Bovine).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:
OC Bovidae: Bovinae: Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-Retina;
RA MEDLINE-96149441; PubMed-8557110;
RT Voelkel H., Beltz E., Klump S., Schultze J.E.;
RT "Cloning and expression of a bovine adenylyl cyclase type VII
RT specific to the retinal pigment epithelium.";
RL FEBS Lett. 378:245-249(1996).
CC -1- FUNCTION: THIS A MEMBRANE-BOUND, CA(2+)-INHIBITABLE ADENYLYL
CC CYCLASE.
CC -1- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE RETINAL PIGMENT
CC EPITHELIUM.
CC -1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: 249806; CAA89894.1; ALT_INIT.
DR HSSP: P26769; IAB8.
DR InterPro: IPR001054; G_cyclase.
DR Pfam: PF00211; guanylate_cyc; 2.
DR SMART: SM00044; CYCC; 2.
DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
DR PROSITE: PS50125; GUANYLATE_CYCLASES_2; 2.
KW Lyase: CAMP synthetase; Transmembrane; Glycoprotein; Repeat.
FT DOMAIN 1 33 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 34 54 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 95 120 POTENTIAL.
FT TRANSMEM 125 145 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 197 594 POTENTIAL.
FT TRANSMEM 595 615 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 620 640 POTENTIAL.
FT TRANSMEM 669 688 POTENTIAL.
FT TRANSMEM 718 737 POTENTIAL.
FT TRANSMEM 746 773 POTENTIAL.
FT TRANSMEM 792 812 POTENTIAL.
FT DOMAIN 813 1078 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 781 781 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1078 AA; 120819 MW; 50E89BF08E37FCBB CRC64;

Query Match 13.5%; Score 61.5; DB 1; Length 1078;
Best Local Similarity 20.9%; Pred. No. 34;
Matches 19; Conservative 19; Mismatches 34; Indels 19; Gaps 2;

OY 4 LITSLIIPISIEHAKTSLSSWKHDQDANVSNMFTSGKLRVGIYYRNADICS 63
DB 739 MSLEKAVLFLVALVAVLVENYPSMOWDCGSHSLGILGTGTL-----SSSSCS 790
OY 64 RHRVTSAGLT-----ODLQWNL 83
DB 791 WHLKTWNTFLVLFYTTLTMLSKQIDYICRL 821

RESULT 14
NUDI_YEAST STANDARD; PRT; 851 AA.
AC P32336; Q08895;
DT 01-OCT-1993 (Rel. 27 Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE NUDI protein.

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GN NUDI OR YOR373W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A.
RA Dulic V., Zanolari B., Riezman H.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Delius H., Hebling U., Hofmann B.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
CC -1- FUNCTION: REQUIRED FOR NUCLEAR DIVISION.
CC -----
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CC -----
DR EMBL: X62147; CAA44073.1; -
DR EMBL: Z75281; CAA9704.1; -
DR PIR: S19056; S19056.
DR SGD: S0005900; NUDI.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 4.
DR PRINTS: PR00019; LEURICHPT.
KW Cell cycle.
FT DOMAIN 223 239 POLY-ASN.
FT DOMAIN 266 274 POLY-SER.
FT CONFLICT 5 6 TQ -> SE (IN REF. 2).
SQ SEQUENCE 851 AA; 94103 MW; CB9F0408633C1315 CRC64;

Query Match 13.4%; Score 61; DB 1; Length 851;
Best Local Similarity 23.5%; Pred. No. 30;
Matches 23; Conservative 14; Mismatches 25; Indels 36; Gaps 4;

OY 9 QLTLLIPISIEHAKTSLSSWKHDQDANVSNMFTSGKLR----- 50
DB 457 QLISILTSKLS-----GSPSYDSDWEKILKVDLSRKLNMGMORLPNVLNLNS 508
OY 51 -----VKGIYYRNADI-CSRRVTSAGLT--ODLQ 78
DB 509 DNEMNTLEGIPSNVVOLEFCSSNKRKITSAGHSLAGFDLE 546

RESULT 15
NUDI_YEAST STANDARD; PRT; 2144 AA.
AC Q12680; Q12290;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE Glutamate synthase [NADPH] precursor (EC 1.4.1.13) (NADPH-GOGAT).
GN GRT1 OR YDL171C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA STRAIN-CN36;
RX MEDLINE-97082505; PubMed-8923741;
RA Filetici P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P.;
RT "Sequence of the GRT1 gene from Saccharomyces cerevisiae reveals the
RT domain structure of yeast glutamate synthase.";
RL Yeast 12:1359-1366(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;

```

RA Pohl T.M.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-oxoglutarate + NADPH.
 CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X89221; CAA61505.1; -;
 CC DR EMBL: Z67750; CAA91574.1; -;
 CC DR EMBL: Z74219; CAA98745.1; -;
 CC DR SGD: S0002330; GLT1.
 CC DR InterPro: IPR002489; DUF14.
 CC DR InterPro: IPR001327; FAD_pyr_redox.
 CC DR InterPro: IPR002932; Glu_synthase.
 CC DR Pfam: PF00070; Pyr_redox; 1.
 CC DR Pfam: PF01493; DUF14; 1.
 CC DR Pfam: PF01643; Glu_synthase; 1.
 CC DR ProDom: PD000139; FAD_pyr_redox; 1.
 CC DR TIGRFAMs: TIGR01317; GOGAT_sm_gam; 1.
 CC KM Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
 KW Glutamate biosynthesis; zymogen.
 FT PROPEP 1 53
 FT CHAIN 54 2144
 FT NP_BIND 1131 1183
 FT METAL 1184 1184
 FT METAL 1190 1190
 FT METAL 1195 1195
 FT METAL 1195 1195
 FT CONFLICT 30 30
 FT CONFLICT 166 172
 FT CONFLICT 449 451
 FT CONFLICT 1752 1752
 SQ SEQUENCE 2144 AA; 238200 MW; 5AA6A948EF95349 CRC64;
 Query Match 13.4%; Score 61; DB 1; Length 2144;
 Best Local Similarity 25.6%; Pred. No. 86;
 Matches 20; Conservative 19; Mismatches 19; Indels 20; Gaps 6;
 QY 5 TLST-QLTLIPSTSHAKTSLSWKHD-----QDANYSNMTFSNGK-----LRVK 52
 Db 348 TSLPEAVMMVPEAYHKMDSDLKAW-YDMAACLMPEWDGPAALTFTDGRYGAIDLDRN 406
 QY 53 GI----YRNAD---ICS 63
 Db 407 GLRPCRYYTSDDRVICA 424

Search completed: December 8, 2002, 19:31:26
 Job time : 24.2774 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 8, 2002, 19:27:28 ; Search time 29.1871 seconds
(without alignments)
286.555 Million cell updates/sec

Title: US-09-880-457-4
Perfect score: 455
Sequence: 1 MALTSLQLILLIPSISH.....TSAGLTLQDQLQMCNLRH 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	67	14.7	296 2 E72203	conserved hypotet
2	67	14.7	307 2 T46103	hypothetical prote
3	66	14.5	286 2 B96615	probable carbonic
4	66	14.5	310 2 JC6516	signal recognition
5	65.5	14.4	641 2 S63645	NADH2 dehydrogenas
6	65	14.3	210 2 T04933	hypothetical prote
7	65	14.3	251 2 C71557	probable ACR - Chl
8	64.5	14.2	276 2 E36990	probable glucanotr
9	64.5	14.2	427 2 F83984	acetylornithine de
10	64	14.1	334 1 S23498	licheninase (EC 3.
11	63.5	14.0	263 1 S31323	orotidine-5'-phosp
12	63.5	14.0	561 2 AG2336	potassium-dependen
13	63.5	14.0	813 2 F83476	probable sideropho
14	63	13.8	119 2 C64174	hypothetical prote
15	63	13.8	345 2 D97407	hypothetical prote
16	63	13.8	345 2 AE2625	conserved hypotet
17	62	13.6	329 2 T47869	hypothetical prote
18	61.5	13.5	1097 2 A29894	isopenicillin N sy
19	61.5	13.5	2145 2 S61041	adenylate cyclase
20	61.5	13.5	455 2 S68685	glutamate synthase
21	61	13.4	851 2 S67285	membrane-bound lyl
22	61	13.4	1101 2 T20881	NOD1 protein - yea
23	61	13.4	277 2 AB1340	maltoedextrose utli
24	60.5	13.3	286 2 H86664	outer membrane lip
25	60.5	13.3	1451 2 A36468	SPF6 protein - yea
26	60	13.2	274 2 AC1866	hypothetical prote
27	60	13.2	283 2 A12836	glycosyl hydrolase
28	60	13.2	301 2 S73347	probable lipoprote
29				

30	60	13.2	354 2 C97614	hypothetical 32.0K
31	60	13.2	785 2 S73098	aminopeptidase (EC
32	59.5	13.1	169 2 D84027	mylodopterin-guan
33	59.5	13.1	216 2 S56421	probable hexulose-
34	59.5	13.1	216 2 D91275	probable hexulose-
35	59.5	13.1	216 2 D86116	probable hexulose-
36	59.5	13.1	277 2 AH1710	maltoedextrose utli
37	59.5	13.1	561 2 T46845	K+-transporting AT
38	59.5	13.1	2391 2 T18410	carbamoyl-phosphat
39	59	13.0	187 2 T15023	hypothetical prote
40	59	13.0	220 1 A27409	CDP diacylglycerol
41	59	13.0	649 2 T22254	hypothetical prote
42	58.5	12.9	769 2 T29796	hypothetical prote
43	58.5	12.9	91 2 AC1998	hypothetical prote
44	58.5	12.9	398 2 AC1998	hypothetical prote
45	58.5	12.9	958 1 JN0102	glucan 1,4-alpha-g

ALIGNMENTS

RESULT 1
E72203
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72203
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72203
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <ARN>
A:Cross-references: GB:AE001822; GB:AE000512; NID:94982429; PIDN:AD36914.1; PID:9498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1852
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1107

Query Match 14.7% Score 67; DB 2; Length 296;
Best local similarity 27.3% Pred. No 5.4;
Matches 15; Conservative 11; Mismatches 19; Indels 10; Gaps 3;

QY 33 DDDM---ANVSNMFTSNGKLRVKG---IYRNADICSHRYTSAGTLQDQLQMC 81
DB 244 EDDWEKFGVPPVNVFSDAMIEYGYVYGAADNC---TALTITPEYKMKMC 294

RESULT 2
T46103
hypothetical protein T25B15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46103
R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Maché, R.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23021
A:Accession: T46103
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <ALC>
A:Cross-references: EMBL:AL132972
A:Experimental source: cultivar Columbia; BAC clone T25B15

C:Genetics:
A:Map position: 3
A:Introns: 63/3; 225/2; 267/3
A>Note: T25B15.100

Query Match 14.7% Score 67; DB 2; Length 307;

Best Local Similarity 18.3%; Pred. No. 5.7;
Matches 15; Conservative 19; Mismatches 26; Indels 22; Gaps 2;

OY 20 HEAKTSLSSMKHDOW-----ANYSNMTEFSNGKRYGITYRN 58
Db 149 HDEYKVLSTYVHNKNEKVRSEHVLVLGARTSMKTKQCHLHLPYSOG-TTNGVLYYC 207
OY 59 ADICSRHRYTSAGTLTLOLQLM 80
Db 208 AMTDDKCVLMSEFDLTSEDVGV 229

RESULT 3

B96615

Probable carbonic anhydrase T18124.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nauen, N.F.; Hughes, B.; Hultar, L.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marshall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzbeg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <STO>
A:Cross-references: GB:AE005173; NID:g11038509; PIDN:AAQ27786.1; GSPDB:GN00141
C:Genetics:
A:Gene: T18124.9
A:Map position: 1

Query Match 14.5%; Score 66; DB 2; Length 286;
Best Local Similarity 21.1%; Pred. No. 6.8;
Matches 27; Conservative 22; Mismatches 29; Indels 50; Gaps 7;

OY 2 AITLSLOLILIPIS-----ISHNAKTSLSW-----KHDOD 35
Db 159 AVTTLOVENTIVGSHNCGIALMSHQHOGSRWNGAKAKLTOLASSHLSFDEQ 218
OY 36 WAN-----VSNM-TFS-----NGKRVKGYIRNADICSRHR-----VTSAGL 72
Db 219 CRNCKESIKDSVNLITYSWTRKVRKGEVKGICYYNLSD-CSELEKMLSDKTYGCF 277
OY 73 TLDDLOLM 80
Db 278 YISDREIW 285

RESULT 4

JC6516

Signal recognition particle protein Sec65 - yeast (Yarrowia lipolytica)
N:Alternate names: SRP19
C:Species: Yarrowia lipolytica, Candida lipolytica
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 23-Jul-1999
R:Sanchez, M.; Beckerlich, J.M.; Gallardín, C.; Dominguez, A.
Gene 203, 75-84, 1997
A:Title: Isolation and cloning of the Yarrowia lipolytica SEC65 gene, a component of the
A:Reference number: JC6516; MUID:96085978; PMID:9426009
A:Accession: JC6516
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <SAS>
A:Cross-references: EMBL:Z22570; NID:g473182; PID:g473183

Query Match 14.5%; Score 66; DB 2; Length 310;

Best Local Similarity 41.5%; Pred. No. 7.5;
Matches 17; Conservative 7; Mismatches 3; Indels 14; Gaps 3;

OY 12 LLLIPISHEAKTSLSSMKHDOWANYSNMTEFSNGKRLVK 52
Db 161 MLTLPST-YEAKHT-----HPKDMAN-----FGHVRVQ 187

RESULT 5

S63645

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Allomyces macrogynus mitochon
C:Species: mitochondrion Allomyces macrogynus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
R:Paquin, B.; Lang, B.F.
J. Mol. Biol. 255, 688-701, 1996
A:Title: The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence
A:Reference number: S63645; MUID:96226032; PMID:8636971
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-641 <PAQ>
A:Cross-references: EMBL:U41288; NID:g1236403; PIDN:AAQ49228.1; PID:g1236411
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Genome: mitochondrion
A:Introns: 144/3; 241/3; 314/1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 14.4%; Score 65.5; DB 2; Length 641;
Best Local Similarity 27.9%; Pred. No. 20;
Matches 19; Conservative 12; Mismatches 28; Indels 9; Gaps 2;

OY 2 AITLSLOLILIPISHEAK-----TSLSSKRWHDOW-----ANYSNMTEFSNGKRLVK 52
Db 522 SLGSLALVLKDPKRMHSIEKPEGLNTVITRMLSKSRFPDNYVTVLIGSLHFG 581
OY 53 GITYRNAD 60
Db 582 GIFARDID 589

RESULT 6

T04933

Hypothetical protein T9A21.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, February 1999
A:Reference number: T04933
A:Accession: T04933
A:Molecule type: DNA
A:Residues: 1-210 <BEV>
A:Cross-references: EMBL:AL021713
A:Experimental source: cultivar Columbia; BAC clone T9A21
C:Genetics:
A:Map position: 4
A:Note: T9A21.160

Query Match 14.3%; Score 65; DB 2; Length 210;
Best Local Similarity 36.0%; Pred. No. 6.2;
Matches 18; Conservative 8; Mismatches 16; Indels 8; Gaps 2;

OY 3 IITLSLOLILIPISHEAKTSLSSMKH-----DQWANSNMTEFS 45
Db 101 IPTNMLPVVGSTIDISPSADKISITIGWHSFDTFOSQSDW-NVTNINVT 149

RESULT 7

C71557

Probable ACR - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: C71557
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A:Reference number: A71570; MUID:J9000809; PMID:9784136
A:Accession: C71557
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <ARN>
A:Cross-references: GB:AEO01284, GB:AEO01273; NID:G3328494; PIDN:ANAC67699.1; PID:G332850
C:Genetics:
A:Experimental source: serotype D, strain UW-3/Cx
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1777

Query Match 14.3%; Score 65; DB 2; Length 251;
Best Local Similarity 26.4%; Pred. No. 7.6; Mismatches 27; Indels 24; Gaps 4;
Matches 23; Conservative 13;

Dy 7 SLGLILLIPSISHEAKTSLSWK--HDQMANVMNTFSNGKLRVKG----- 54
||| | : || | : || | : || | : || | : || | : || | : || | :
Db 91 NIQLIAYHLP---DAFTTGNMKVKARDLGEQLESQSPSLGVXGPPEMEVHDFI 147

Dy 55 -----YYRNADIC----SRHRVTSAGL 72
|| | : || | : || | : || | : || | : || | : || | : || | :
Db 148 SQLSAVYQTPLAKALGGKKRVSSAAL 174

RESULT 8
E96990
probable glucanotransferase (endo alpha-1,4 polygalactosaminidase related protein) [Impc
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E96990
R:Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daily, M.J.; Bennett, G.N.; Koornik, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clq
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E96990
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <KUN>
A:Cross-references: GB:AEO01437; PIDN:AAK78712.1; PID:G15023617; GSPDB:GM00168
C:Genetics:
A:Experimental source: Clostridium acetobutylicum ATCC824
A:Gene: CAC0736

Query Match 14.2%; Score 64.5; DB 2; Length 276;
Best Local Similarity 30.5%; Pred. No. 9.7; Mismatches 15; Indels 11; Gaps 4;
Matches 18; Conservative 15;

Dy 29 SMKHPDWMNVSMPTFSTN-----GR-LRYKGI--YYRNADICSRRHVTSAGLTLDL 77
||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
Db 105 NMK-DSMWIDVSNLKMDNYVVYTLGNKLKNKGVDGFELDNLDVYSKYKDSMFGLINI 162

RESULT 9
F83984
acetylornithine deacetylase BH2678 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
C:Accession: F83984
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiro
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: F83984
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <STO>

```
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA06397.1; GSPDB:G  
C:Genetics:  
A:Gene: BH2678  
C:Superfamily: succinyl-diaminopimelate desuccinylase
```

	Query Match	14.2%	Score 64.5;	DB 2;	Length 427;
	Best Local Similarity	27.2%;	Pred. No. 16;	Indels 41;	Gaps 2;
Matches	22;	Conservative 13;	Mismatches		

OY 7 SIQILILLIPISIEAHKTSLSQWKHODPW---ANVSNMTFSNGKLRVKGIVRNADICS 63
 ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 347 AVOLLEKKIHYHLGTGEVRKSMSOTVTDDGGWLAAAG-IPTLLFGCKLEDASHVEEELIAE 406
 : | ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 64 RHRVTSAGLTLODLWCNLIR 84
 : | ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 407 LVQYTKLTLTF--IYEWCCLR 425

```
RESULT 10  
S23498  
licheninase (EC 3.2.1.73) l1cb precursor - Clostridium thermocellum  
N:Alternate names: beta-1,3-1,4-glucanase l1cb; lichenase l1cb  
C:Species: Clostridium thermocellum  
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999  
C:Accession: S23498; S22137  
R:Schlimming, S.; Schwarz, W.H.; Staendenbauer, W.L.  
Eur. J. Biochem. 204, 13-19, 1992  
F:Title: Structure of the clostridium thermocellum gene l1cb and the encoded beta-1,3  
l cellulases.  
A:Reference number: S23498; MUID:9215194; PMID:1740123  
A:Accession: S23498  
A:Molecule type: DNA  
A:Residues: 1-334 <SCGH>  
A:Cross-references: EMBL:X63355; NID:g40697; PIDN:CAA44959.1; PID:g40698  
C:Genetics:

A:Gene: l1cb  
C:Superfamily: licheninase l1cb; clostridium cellulase repeat homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:1-27/Domain: signal sequence #status predicted <STC>  
F:28-334/Product: licheninase #status predicted <MAT>  
F:273-226/Domain: clostridium cellulase repeat homology <CCR1>  
F:308-331/Domain: clostridium cellulase repeat homology <CCR2>



|         | Query Match           | 14.1%            | Score 64;     | DB 1; | Length 334; |
|---------|-----------------------|------------------|---------------|-------|-------------|
|         | Best Local Similarity | 27.8%;           | Pred. No. 14; |       |             |
| Matches | 20;                   | Conservative 13; | Mismatches    | 15;   | Indels 24;  |
|         |                       |                  |               |       | Gaps 3;     |



OY    1 MALITSLDQLILLIPSIEHAHKTSL-----SSWKHDQDMAN----- 38  
       ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db    6 ISLMASTLVSVIAYPRYKAATVNTPFVAVFNSNDSSQWE-KADMANGSVENCWA 64



OY    39 -VSNMFTSNGKL 49  
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db    65 KPSQVFESNGKM 76



```
RESULT 11
S31323
orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (Pichia angusta)
C:Species: Pichia angusta
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000
C:Accession: S31323
R:Reichelbach, A.; Goedecke, S.; Janowicz, Z.A.; Hollenberg, C.P.
submitted to the EMBL Data Library, November 1992
A:Description: Cloning and sequencing of the URA3 locus of the methylotrophic yeast H
A:Reference number: S31323
A:Accession: S31323
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-263 <EMR>
A:Cross-references: EMBL:X69461; NID:g2783; PIDN:CAA49221.1; PID:g2784
C:Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylyse
```


```

C:Keywords: carbon-carbon lyase; carboxy-lyase
F:3-263/Domain: orotidine-5'-phosphate decarboxylase homology <OPD>

Query Match 14.0%; Score 63.5; DB 1; Length 263;
Best Local Similarity 39.5%; Pred. No. 12;
Matches 17; Conservative 7; Mismatches 12; Indels 7; Gaps 2;

QY 33 DDMANVSNMFTSGKLRVKGITYRN---ADICSRHRYVTSAGL 72
DB 90 DRKFADIGNTV---KLOYKGGIYRTSKRADITNMGVYAGGI 128

RESULT 12

AG2336
potassium-dependent ATPase chain A [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AG2336

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:11595285; PMID:11759840
A:Accession: AG2336

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1561 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA075945.1; PID:g17133381; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:

A:Gene: at14246
C:Superfamily: H+/K+-transporting ATPase chain A
Query Match 14.0%; Score 63.5; DB 2; Length 561;
Best Local Similarity 30.1%; Pred. No. 29;
Matches 25; Conservative 11; Mismatches 32; Indels 15; Gaps 3;

QY 1 MAILTSLQILIPISHEAKTSLSSWKHODMANVSNMFTSGKLRVKGITYRNAD 60
DB 415 LAILLIPHYIVLIPISALALAPFSL-----GISNPSFHC-----ISQVVEYAS 461

QY 61 TCSRHVTSAGTLTDLQDLQCNL 83
DB 462 ASANNGSGLEGLT--DNSLWMNL 482

RESULT 13

F83476
probable siderophore receptor PA1365 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83476

R:Stover, C.K.; Plam, X.Q.; Ertwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83476

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-813 <STO>
A:Cross-references: GB:AE004565; GB:AE004091; NID:g9947294; PIDN:AA0454.1; GSPDB:GN00179
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1365

Query Match 14.0%; Score 63.5; DB 2; Length 813;
Best Local Similarity 28.8%; Pred. No. 44;
Matches 19; Conservative 11; Mismatches 23; Indels 13; Gaps 3;
QY 25 TSLSWKHDDMANVSNMFTSNCK-LRVKGI-----YRNADICSRHRYT---SAG 71

DB 711 TAYLOKRPADPMNRLQATFFDSKDYRLDGVSEGRROYSTYTVDLVDSQYRITPPDQLS 770
QY 72 LITLQDL 77
DB 771 LGIQLN 776

RESULT 14

CG4174
hypothetical protein H1656 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C:Accession: CG4174

R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kellavagge, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: CG4174

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <TIGR>
A:Cross-references: GB:U32838; GB:L42023; NID:g1574497; PIDN:AA023300.1; PID:g1574505
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Superfamily: hypothetical protein H1656

Query Match 13.8%; Score 63; DB 2; Length 119;
Best Local Similarity 21.9%; Pred. No. 5.5;
Matches 16; Conservative 19; Mismatches 28; Indels 10; Gaps 3;

QY 10 LILIPISHEAKTSLSS--WKHODMANVSNMFTSGKLRVKGITYRNADICSRHY 67
DB 49 IVEVEVQRSHAVGSAIESVDNRKQKWDANLWIAKONMSLE-----DANCRFDL 101

QY 68 TSAGLTQDLQDL 80
DB 102 IAFGKTPDQIDQ-W 113

RESULT 15

D97407

hypothetical protein AGR_C-701 [imported] - Agrobacterium tumefaciens (strain C58, Ce)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: D97407

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; PMID:11743194
A:Accession: D97407

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <KUR>
A:Cross-references: GB:AA007869; PIDN:AAK6213.1; PID:g15155314; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C-701
A:Map position: circular chromosome

Query Match 13.8%; Score 63; DB 2; Length 345;
Best Local Similarity 28.0%; Pred. No. 19;
Matches 21; Conservative 14; Mismatches 20; Indels 20; Gaps 5;

QY 12 LILIPISHEAKTSLSSWKHODMANVSNMFTSGKLRVKGITYRNADI-----C 62
DB 144 LTMVPSFVHEL-DVSIPT---PEMGRTV-MDISYG-----GIFYALVDVQIGLTTEKA 192

QY 63 SRHRTSAGTLTDL 77
DB 193 NAKLVAAAGMTLAKDL 207

Tue Dec 10 10:51:41 2002

us-09-880-457-4.rpt

Page 5

Search completed: December 8, 2002, 19:34:43
Job time : 37.1871 secs

2
1
2

Tue Dec 10 10:51:40 2002

us-09-880-457-4.ra1

Page 1

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OM protein - protein search, using sw model

Run on: December 8, 2002, 19:30:43 : Search time 18.5226 Seconds
(without alignments)
138.199 Million cell updates/sec

Title: US-09-880-457-4

Perfect score: 455
Sequence: 1 MAILTSLQILLLIPSIH.....TSAGLTLDLQIMCRLRIH 87

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, AA:
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6CTUS.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180.5	39.7	317	3	US-08-996-139-13
2	180.5	39.7	317	4	US-08-995-659-13
3	180.5	39.7	317	4	US-09-215-649A-13
4	180.5	39.7	317	4	US-09-052-521C-4
5	180.5	39.7	317	4	US-09-577-780-13
6	176	38.7	294	3	US-08-996-139-11
7	176	38.7	294	4	US-08-995-659-11
8	176	38.7	294	4	US-09-215-649A-11
9	176	38.7	294	4	US-09-577-780-11
10	176	38.7	316	2	US-08-842-842-7
11	176	38.7	316	4	US-08-989-362-2
12	176	38.7	316	4	US-09-052-521C-2
13	176	38.7	28	4	US-09-052-521C-34
14	14.9	12.6	6	5206163-1	Sequence 6, Appl
15	67.5	14.8	490	4	US-09-336-643A-6
16	64	14.1	279	3	US-09-286-690-9
17	63	13.8	376	1	US-09-052-521C-33
18	63	13.8	376	1	US-08-594-031-100
19	63	13.8	376	1	US-08-594-031-102
20	61.5	13.5	329	1	US-09-413-231-5
21	61.5	13.5	329	4	US-08-618-911-6
22	60.5	13.3	158	2	US-08-618-911-6
23	60	13.2	721	4	US-09-184-748-2
24	59.5	13.1	2391	2	US-08-446-855A-2
25	59.5	13.0	2391	2	US-09-150-741-2
26	59	13.0	2391	2	US-08-763-121-4
27	59	13.0	220	4	US-09-216-066-4

ALIGNMENTS

28	57.5	12.6	525	1	US-08-077-939-17	Sequence 17, Appl
29	57.5	12.6	525	1	US-08-461-599-17	Sequence 17, Appl
30	57.5	12.6	525	1	US-08-461-621-17	Sequence 17, Appl
31	57.5	12.6	525	1	US-08-465-334-17	Sequence 17, Appl
32	56.5	12.4	158	3	US-08-618-911-4	Sequence 4, Appl
33	56.5	12.4	158	3	US-08-938-675A-2	Sequence 10, Appl
34	56.5	12.4	333	4	US-09-413-231-10	Sequence 4, Appl
35	56	12.3	391	4	US-09-200-090-4	Sequence 1, Appl
36	56	12.3	521	2	US-08-933-227-1	Sequence 1, Appl
37	56	12.3	878	4	US-08-735-934A-2	Sequence 93, Appl
38	55.5	12.2	81	2	US-08-332-562A-93	Sequence 16, Appl
39	55.5	12.2	146	4	US-08-637-323-16	Sequence 3, Appl
40	55.5	12.2	149	3	US-08-584-031-16	Sequence 3, Appl
41	55.5	12.2	151	1	US-07-940-605A-3	Sequence 2, Appl
42	55.5	12.2	151	2	US-08-690-096-3	Sequence 8, Appl
43	55.5	12.2	261	1	US-07-940-605A-2	Sequence 2, Appl
44	55.5	12.2	261	1	US-08-184-422-8	Sequence 2, Appl
45	55.5	12.2	261	1	US-08-360-923A-2	Sequence 2, Appl

RESULT 1
US-08-996-139-13
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996, 139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064, 671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813, 509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772, 330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

Query Match 39.7%; Score 180.5; DB 3; Length 317;
Best Local Similarity 59.7%; Pred. No. 3.4e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKTSLSSMKHDODMANVSNMTFSGKLRK--GIYRNADICSRHRTSAGL 72
DB 175 IPSSG---HKVSLSSWYHDRGMAKISNMTFSGKLIYNQDGFYLYANICFRHHTSGDL 231

QY 73 TLQDLQL 79
DB 232 ATEYLQL 238

RESULT 2
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; APPLICATION NUMBER: USN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; CLASSIFICATION:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; APPLICATION DATA:
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-13

Query Match 39.7%; Score 180.5; DB 4; Length 317;
Best Local Similarity 59.7%; Pred. No. 3.4e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKTSLSSMKHDODMANVSNMTFSGKLRK--GIYRNADICSRHRTSAGL 72
DB 175 IPSSG---HKVSLSSWYHDRGMAKISNMTFSGKLIYNQDGFYLYANICFRHHTSGDL 231

QY 73 TLQDLQL 79
DB 232 ATEYLQL 238

RESULT 3
US-09-215-649A-13
; Sequence 13, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

Query Match 39.7%; Score 180.5; DB 4; Length 317;
Best Local Similarity 59.7%; Pred. No. 3.4e-15;
Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

QY 15 IPSISHEAKTSLSSMKHDODMANVSNMTFSGKLRK--GIYRNADICSRHRTSAGL 72
DB 175 IPSSG---HKVSLSSWYHDRGMAKISNMTFSGKLIYNQDGFYLYANICFRHHTSGDL 231

QY 73 TLQDLQL 79
DB 232 ATEYLQL 238

RESULT 4
US-09-052-521C-4
; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:

FEEDBACK: (2007-2008)
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids

Query Match	38.78;	Score 176;	DB 3;	Length 294;
Best Local Similarity	55.48;	Pred. No. 1,2e-14;		
Matches	36;	Mismatches	21;	Indels 2;
				Gaps 1

QY 17 SISHEAKTSLSSWKHDODMANVNTFSNGKLRV--GIYYRNADICSRHRTSAGTL 74
Db 151 SIPSGSHKVTLSWYHDKRMAKISNMTLNGLRVNODGFYLYANICFRHHTSGSVPT 210
QY 75 QDLQL 79
Db 211 DYLOL 215

RESULT 7

US-08-995-659-11
Sequence 11, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-995-659-11

Query Match 38.7%; Score 176; DB 4; Length 294;
Best Local Similarity 55.4%; Pred. No. 1,2e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 17 SISHEAKTSLSSWKHDODMANVNTFSNGKLRV--GIYYRNADICSRHRTSAGTL 74
Db 151 SIPSGSHKVTLSWYHDKRMAKISNMTLNGLRVNODGFYLYANICFRHHTSGSVPT 210
QY 75 QDLQL 79
Db 211 DYLOL 215

RESULT 8

US-09-215-649A-11
Sequence 11, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 38.7%; Score 176; DB 4; Length 294;
Best Local Similarity 55.4%; Pred. No. 1,2e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 17 SISHEAKTSLSSWKHDODMANVNTFSNGKLRV--GIYYRNADICSRHRTSAGTL 74
Db 151 SIPSGSHKVTLSWYHDKRMAKISNMTLNGLRVNODGFYLYANICFRHHTSGSVPT 210
QY 75 QDLQL 79
Db 211 DYLOL 215

RESULT 9

US-09-577-780-11
Sequence 11, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB


```

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSR 08/772,330
FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-577-780-11

Query Match          38.7%; Score 176; DB 4; Length 294;
Best Local Similarity 55.4%; Pred. No. 1,2e-14;
Matches    36; Conservative   6; Mismatches    21; Indels     2; Gaps      1;

QY       17 SISHEAKTSLSSMKRHDQDWMVSNMTSNGKLRVK--GIYRNADICSRHRYTSAGTL 74
           || :||| | | | :| :||| | | | | | | | | | | | | | | | | | | :
Db        151 SIPSGSHKVTLSMWHRGMAKISNMNTLSNGKLRVNODGFYLYANICPRHHTSGSVPT 210

QY       75 QDLQL 79
           |||
Db        211 DYQLL 215

RESULT 10
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-842-7

Query Match      38.7%  Score 176;  DB 2;  Length 316;
Best Local Similarity 55.4%  Pred. No. 1.3e-14;
Matches 36;  Conservative 6;  Mismatches 21;  Indels 2;  Gaps 1.

QY      17  SISSEAHKTLSSMKHODDMANYSNMATESNGKLRVK--GIYYRNADICSRHRYTSAGLT 74
      11  :::::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::|||||:::|:::
Db      173  SIPEGSHKAYLLSSWYHDRCMAKISNMTLSNGKLRVYNOGFFYLVAICFRHHTSGSVPT 232

QY      75  QDLQL 79
      111
Db      233  DYQL 237

RESULT 11
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Mattson, Jeanine D.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,050
; REFERENCE/DOCKET NUMBER: DX0586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-362-2

Query Match      38.7%  Score 176;  DB 4;  Length 316;

```

Best Local Similarity 55.4%; Pred. No. 1.3e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 17 SISHEAKTSLSSMKHODMANVSNMTPFSNGKLRVK--GIYYRNADICSRHRTSAGLTL 74

Db 173 SIPSQSHKVTLSWYHNRGMAKISNMTLSNGKLRVNODGFYLYANICFRHHTSGSVPT 232

QY 75 QDLQL 79

Db 233 DYQL 237

RESULT 12

US-09-052-521C-2
Sequence 2, Application US/09052521C
Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.

TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors

FILE REFERENCE: A-451BIV

CURRENT APPLICATION NUMBER: US/09/052,521C

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 08/880,855

PRIOR FILING DATE: 1997-06-23

PRIOR APPLICATION NUMBER: 08/842,842

PRIOR FILING DATE: 1997-04-16

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 316

TYPE: PRT

ORGANISM: Mouse

US-09-052-521C-2

Query Match 38.7%; Score 176; DB 4; Length 316;
Best Local Similarity 55.4%; Pred. No. 1.3e-14;
Matches 36; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

QY 17 SISHEAKTSLSSMKHODMANVSNMTPFSNGKLRVK--GIYYRNADICSRHRTSAGLTL 74

Db 173 SIPSQSHKVTLSWYHNRGMAKISNMTLSNGKLRVNODGFYLYANICFRHHTSGSVPT 232

QY 75 QDLQL 79

Db 233 DYQL 237

RESULT 13

US-09-052-521C-34
Sequence 34, Application US/09052521C
Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.

TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors

FILE REFERENCE: A-451BIV

CURRENT APPLICATION NUMBER: US/09/052,521C

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 08/880,855

PRIOR FILING DATE: 1997-06-23

PRIOR APPLICATION NUMBER: 08/842,842

PRIOR FILING DATE: 1997-04-16

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 34

LENGTH: 28

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-052-521C-34

Query Match 16.7%; Score 76; DB 4; Length 28;

Best Local Similarity 54.2%; Pred. No. 0.0037;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 17 SISHEAKTSLSSMKHODMANVSNMTPFSNGKLRVK--GIYYRNADICSRHRTSAGLTL 74

Db 4 SIPSQSHKVTLSWYHNRGMAKISNMTLSNGKLRVNODGFYLYANICFRHHTSGSVPT 27

RESULT 14

US-09-052-521C-1
Patent No. 5206163

APPLICANT: RENARD, ANDRE;DINA, DINO;MARTIAL, JOSEPH

TITLE OF INVENTION: DNA ENCODING BOVINE DIARRHEA

VIRUS PROTEIN

NUMBER OF SEQUENCES: 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/550,816

FILING DATE: 06-JUL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 331,037

FILING DATE: 29-MAR-1989

APPLICATION NUMBER: 752,981

FILING DATE: 08-JUL-1985

SEQ ID NO:1

LENGTH: 1286

5206163-1

Query Match 14.9%; Score 68; DB 6; Length 1286;
Best Local Similarity 23.4%; Pred. No. 6.1e-14;
Matches 25; Conservative 18; Mismatches 22; Indels 42; Gaps 4;

QY 1 MAILSLQTL-----LILPISH-----EAKHTSLSSMKHQ 34

Db 1196 MAVTLTLMISTYDYRRYKMLQCLISLAGVFLIRSLKHLGEIPELTPWRR--- 1252

QY 35 DWANVSNMTPFSNGKLRVKGIYYRNADICSRHRTSAGLTLQIMC 81

Db 1253 -----PLTFL-----LTLTATVYTRKWKVDIAGILLOGPQSF 1286

RESULT 15

US-09-336-643A-6
Sequence 6, Application US/09336643A
Patent No. 6399761

GENERAL INFORMATION:

APPLICANT: Miller, Andrew P.

APPLICANT: Curran, Mark Edward

APPLICANT: Hu, Ping

APPLICANT: Rutger, Marc

APPLICANT: Wang, Jian-Wang

TITLE OF INVENTION: No. 6399761el Human Potassium Channels

FILE REFERENCE: SEQ-15P

CURRENT APPLICATION NUMBER: US/09/336,643A

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR FILING DATE: 1998-08-07

PRIOR APPLICATION NUMBER: 60/116,448

PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: PCT/US99/03826

PRIOR FILING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 490

TYPE: PRT

ORGANISM: H. sapiens

US-09-336-643A-6

Query Match 14.8%; Score 67.5; DB 4; Length 490;
Best Local Similarity 22.0%; Pred. No. 2e-14;
Matches 20; Conservative 16; Mismatches 30; Indels 25; Gaps 3;

QY 1 MAILSLQTLILPISHAKHTSLSS-----WKHODMANVSNMTPFSNGKLRVKGIY 55

Db 328 LFLSVGISIFSVLYISVEKDHFTSSLTSLPICW-----WATISMVTYVG----- 374
Qy 56 YRNADICSRHRYTSAGLTLQDLQLMCNLRIT 86
Db 375 -----DTHPVTLAGKLIASCTICGILYV 398

Search completed: December 8, 2002, 19:35:31
Job time : 20.5226 secs

11

Tue Dec 19 10:51:39 2002

us-09-880-457-4.rag

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Run on: December 8, 2002, 17:26:33 : Search time 52.7613 seconds
(without alignments)
219.722 Million cell updates/sec

OM protein - protein search, using sw model

Title: US-09-880-457-4
Perfect score: 1 MAILTSLIQLILLIPSIH.....TSAGITLQDLQMCNLRIT 87
Sequence: BLOSUM62, Gapop 10.0, Gapext 0.5

Scoring table: 908470 seqs, 133250620 residues 908470

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Minimum Match 0%
Maximum Match 100%

Post-processing: Minimum Match 0%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the total score distribution.
and is derived by analysis of

SUMMARIES

Description

Result NO.	Score	Query Length	ID	Description
1	440	96.7	95	AAU83632 Human PRO protein,
2	181	39.7	170	AAU83632 Human FLAG-murine
3	180.5	39.7	152	AAU83632 Human acid sequenc
4	180.5	39.7	160	AAU83632 Human PRO206 polyp
5	180.5	39.7	244	AAU83632 Human TRANCE prote
6	180.5	39.7	246	AAU83632 Human osteoprotege
7	180.5	39.7	317	AAU83632 Human osteoclasto
8	180.5	39.7	317	AAU83632 Human osteoclasto
9	180.5	39.7	317	AAU83632 Human osteoclasto
10	180.5	39.7	317	AAU83632 Human osteoclasto

11	180.5	39.7	317	AAU83632
12	180.5	39.7	317	AAU83632
13	180.5	39.7	317	AAU83632
14	180.5	39.7	317	AAU83632
15	180.5	39.7	317	AAU83632
16	180.5	39.7	317	AAU83632
17	180.5	39.7	317	AAU83632
18	180.5	39.7	317	AAU83632
19	180.5	39.7	317	AAU83632
20	180.5	39.7	317	AAU83632
21	180.5	39.7	317	AAU83632
22	180.5	39.7	317	AAU83632
23	180.5	39.7	317	AAU83632
24	180.5	39.7	317	AAU83632
25	180.5	39.7	317	AAU83632
26	180.5	39.7	317	AAU83632
27	180.5	39.7	317	AAU83632
28	180.5	39.7	317	AAU83632
29	180.5	39.7	317	AAU83632
30	180.5	39.7	317	AAU83632
31	180.5	39.7	317	AAU83632
32	180.5	39.7	317	AAU83632
33	180.5	39.7	317	AAU83632
34	180.5	39.7	317	AAU83632
35	180.5	39.7	317	AAU83632
36	180.5	39.7	317	AAU83632
37	180.5	39.7	317	AAU83632
38	180.5	39.7	317	AAU83632
39	180.5	39.7	317	AAU83632
40	180.5	39.7	317	AAU83632
41	180.5	39.7	317	AAU83632
42	180.5	39.7	317	AAU83632
43	180.5	39.7	317	AAU83632
44	180.5	39.7	317	AAU83632
45	180.5	39.7	317	AAU83632

ALIGNMENTS

RESULT 1
AAU83632 standard: protein: 95 AA.
AAU83632: (first entry)
08-MAY-2002 (first entry)
Human PRO protein, Seq ID NO 82.
Human: secreted protein; PRO: tumour; lung cancer; colon cancer;
breast cancer; prostate tumour; rectal tumour; liver tumour;
pericyte cell proliferation; chondrocyte cell proliferation;
tumour necrosis factor-alpha.
Homo sapiens.
WO200208288-A2.
31-JAN-2002.
29-JUN-2001: 2001WC-US21066.
20-JUL-2000: 2000US-219556P.
20-JUL-2000: 2000US-220585P.
25-JUL-2000: 2000US-220605P.
25-JUL-2000: 2000US-220607P.
25-JUL-2000: 2000US-220624P.
25-JUL-2000: 2000US-220638P.
25-JUL-2000: 2000US-220648P.
25-JUL-2000: 2000US-220666P.
25-JUL-2000: 2000US-220683P.
25-JUL-2000: 2000US-220893P.
28-JUL-2000: 2000WO-US20710.

NF-KB receptor act
Amino acid sequenc
Human receptor act
Human full-length
Human TRANCE prote
Human TRANCE dif
Rat osteoclast Hom
Human TRANCE
Amino acid sequenc
Amino acid sequenc
DNA encoding
An osteoprotegerin
Amino acid sequenc
An osteoprotegerin
An osteoprotegerin
NF-KB receptor act
NF-KB receptor act
Murine receptor ac
Murine receptor (re
Murine TRANCE
Human osteoprotege
Human osteoprotege
Amino acid seq
Murine TRANCE
Mouse OBM protein
Amino acid sequenc
Amino acid sequenc
Mouse TRANCE prote
GlutathioneS-transf
Murine GST-modp fu
Amino acid sequenc
Mouse OBM protein
An osteoprotegerin

PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23522.
 PR 15-SEP-2000; 2000MO-US23522.
 PR 10-NOV-2000; 2000MO-US23522.
 PR 28-NOV-2000; 2000MO-US23522.
 PR 01-DEC-2000; 2000MO-US23522.
 PR 20-DEC-2000; 2000MO-US23522.
 PR 20-DEC-2000; 2000MO-US23522.
 PR 28-FEB-2001; 2001MO-US054280.
 PR 10-MAY-2001; 2001MO-US054280.
 PR 25-MAY-2001; 2001MO-US054280.
 PA (GETH) GENENTECH INC.
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT,
 DR WPI: 2002-172001/22.
 DR N-PSDB; ABR33576.
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumour,
 PT tumour or liver tumour -
 PS Claim 11: Figure 82; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polypeptides
 CC are listed in the accompanying sequences. The PRO polypeptides are
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast cancer, prostate tumour, rectal tumour,
 CC liver tumour, cancer, breast tumour, prostate tumour, rectal tumour or
 CC the proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the release of tumour necrosis factor- α cells, for stimulating the
 CC weight loss of, or inhibiting the proliferation of human dermal
 CC adipocytes. The PRO polypeptide may also be used as a molecular
 CC and in chromosome and gene mapping, including use as hybridisation probes,
 CC protein sequences of the invention. AA083592-AA083713 represent human PRO
 SO Sequence 95 AA:
 Query Match
 Best Local Similarity 96.7%; Score 440; DB 23; Length 95;
 Matches 84; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 MAILTSLQILLIPSHRAKTSLSWKHDQMANVSNMTFSGKLRVKGITYRNAD 60
 DB 1 MAILTSLQILLIPSHRAKTSLSWKHDQMANVSNMTFSGKLRVKGITYRNAD 60
 OY 61 ICSRRHRTSAGLTLDLQMCNLRIT 86
 DB 61 ICSRRHRTSAGLTLDLQMCNLRIT 86
 RESULT 2
 AA08386 standard; Protein, 170 AA.
 AC AA08386;
 AC 17-DEC-2001 (first entry)
 DE Mouse FLAG-murine Opcbp[158-316].
 KW Antibody; Opcbp; osteoprotegerin; FLAG-murine Opcbp[158-316];
 KW osteoprotegerin binding protein; osteoclast formation;
 KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
 KW bone cancer; Rheumatoid arthritis; hypercalcaemia of malignancy;

KW Steroid-induced osteoporosis; mutant; mutein.
 OS Mus sp.
 OS Synthetic.
 FH Key
 FT Peptide
 FT Misc-difference
 FT 83..87
 FT /label= flag-tag
 FT /note= "Note wild-type Ser-Val-Pro-Thr-Asp
 PN substituted by Asp-Leu-Ala-Thr-Glu"
 PD W0200162932-A1.
 PP 30-AUG-2001.
 PR 23-FEB-2001; 2001MO-US05973.
 PR 23-FEB-2001; 2000US-0511139.
 PR 22-FEB-2001; 2001US-0791153.
 PA (AMGE-) AMGEN INC.
 PI Deshpande RV, Hiltz A, Boyle WJ, Sullivan JK,
 PI WPI: 2001-557706/62.
 DR N-PSDB; AAS13369.
 CC Antibodies that bind antagonistically to osteoprotegerin binding
 CC protein, useful for treating osteoporosis, metastasis of cancer to
 CC steroid-induced osteoporosis, hypercalcaemia of malignancy and
 CC Example 10; Fig 28; 239pp; English.
 CC The invention relates to an antibody or antigen binding domain (or
 CC fragment, variant or derivative) which binds to an osteoprotegerin
 CC binding protein (Opcbp) and which is an antagonistic antibody (or
 CC osteoclast formation or activation domain may be administered to
 CC prevent or treat loss of bone mass in a mammal and to prevent or treat
 CC osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
 CC hypercalcaemia of malignancy and cancer to bone, rheumatoid arthritis,
 CC present sequence encodes FLAG-murine Opcbp[158-316].
 SO Sequence 170 AA:
 Query Match
 Best Local Similarity 39.8%; Score 181; DB 22; Length 170;
 Matches 37; Conservative 6; Mismatches 20; Indels 2; Gaps 1;
 OY 17 SISRAHRTSLSSWKHDQMANVSNMTFSGKLRV--GIYRNADICSRRHRTSAGLT 74
 DB 27 SIPSGSHKVTLSWYHDGMAKISNMTLSGKLRVWDGFFYLIANICFRHETSGDGLAT 86
 OY 75 ODLOL 79
 DB 87 EYLOL 91
 RESULT 3
 AAB67248 standard; Protein, 152 AA.
 AC AAB67248;
 AC 18-APR-2001 (first entry)
 DE Human RANKL.
 KW Human; Apo2 ligand: divalent metal ions; viral infection; cancer.

OS Homo sapiens.
 XX WO200100832-A1.
 XX
 XX
 PD 04-JAN-2001.
 XX
 XX 26-JUN-2000; 2000WO-US17579.
 XX
 XX 28-JUN-1999; 99US-0141342.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Hymowitz S, Kelley RE, Koumenis I, Leung S;
 PI O'Connell M, Pal R, Shahrokh Z, Simmons L;
 XX
 XX WPI; 2001-123012/13.
 XX
 XX Use of divalent metal ions for making Apo-2 ligand and in formulations
 PT containing Apo-2 ligand for increasing yield and stability of ligand
 PT trimers, useful for therapeutic applications -
 XX
 XX Disclosure; Fig 3; 60pp; English.
 XX
 CC The present invention relates to a formulation comprising Apo-2
 CC ligand and divalent metal ions. Apo-2 ligand and the formulation
 CC are useful for treating cancers and viral infections. Addition
 CC of divalent metal ions for making Apo-2 ligand and formulations
 CC containing Apo-2 ligand results in increased yield and stability
 CC of Apo-2 ligand trimers.
 XX
 XX Sequence 152 AA:
 SQ
 Query Match 39.7%; Score 180.5; DB 22; Length 152;
 Best Local Similarity 59.7%; Pred. No. 8, 1e-15;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 QY 15 IPSISHEAKHTSLSSWKHDQDMANVSNMTPSNGKLRVK--GIYYRNADICSRHRTVSAGL 72
 DB 13 IPSGS---HKVSLSSWYHGRGMAKISNMTFSNGKLIYNDGFYLYANICFRHHTSGDL 69
 QY 73 TLQDLQ 79
 DB 70 ATEYLQ 76
 DE Amino acid sequence of a human TNF ligand QPGL.
 XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX
 OS Homo sapiens.
 XX WO200047740-A2.
 XX
 PD 17-AUG-2000.
 XX
 XX 11-FEB-2000; 2000WO-US03653.
 XX
 XX 12-FEB-1999; 99US-0119906.
 PR 18-NOV-1999; 99US-0166271.
 XX
 XX (AMGE-) AMGEN INC.

PI Boyle WJ, Hsu H;
 XX WPI; 2000-558217/51.
 XX
 XX
 DR Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 XX
 XX Claim 14; Fig 9; 71pp; English.
 XX
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 XX
 XX Sequence 160 AA:
 SQ
 Query Match 39.7%; Score 180.5; DB 21; Length 160;
 Best Local Similarity 59.7%; Pred. No. 8, 7e-15;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 QY 15 IPSISHEAKHTSLSSWKHDQDMANVSNMTPSNGKLRVK--GIYYRNADICSRHRTVSAGL 72
 DB 18 IPSGS---HKVSLSSWYHGRGMAKISNMTFSNGKLIYNDGFYLYANICFRHHTSGDL 74
 QY 73 TLQDLQ 79
 DB 75 ATEYLQ 81
 DE Human PRO206 polypeptide.
 XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukemia; neuronal disorder; stromal disorder; blastocoeleic disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW cytostatic; neuroprotective.
 XX
 OS Homo sapiens.
 XX WO200153486-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 11-FEB-2000; 2000WO-US03655.
 XX
 XX 08-MAR-1999; 99WO-US05028.
 PR 11-MAR-1999; 99US-123972P.
 PR 11-MAY-1999; 99US-133459P.
 PR 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-140650P.
 PR 22-JUN-1999; 99US-140653P.
 PR 20-JUL-1999; 99US-144758P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 17-AUG-1999; 99US-149385P.
 PR 31-AUG-1999; 99US-151689P.
 PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan RJ,
 PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM,
 PI Watanabe CK, Wood WT;
 DR WPI: 2002-205567/26.
 DR N-PSDB; ABR40274.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for
 PT treating benign or malignant tumours, leukaemias and lymphoid
 PT malignancies, inflammatory, angiogenic and immunologic disorders -
 XX
 PS Claim 61; Fig 42; 302pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,
 CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
 CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
 CC macrophagal, stromal and blastocoele disorders, inflammatory, immune
 CC and angiogenic disorders. The polynucleotide sequences are also
 CC useful in gene therapy. AA086128-AA086162 represent the human PRO
 CC polypeptides of the invention.
 CC
 SO Sequence 244 AA;
 Query Match 39.7%; Score 180.5; DB 23; Length 244;
 Best Local Similarity 59.7%; Pred. No. 1.5e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 OY 15 IPSISHEAKRTSLSSWKHDQDANVSNMTFSNGKLRV--GIYRRNADICSRHRTVSAGL 72
 DB 102 IPSGS---HKVSLSSWYHDMGNAKISNMTFSNGKLIYNODGFYLVANICFRHHTSGDL 158
 OY 73 TLQDPLQ 79
 DB 159 ATEYLQL 165
 RESULT 6
 AA078286
 ID AAU78286 standard; Protein; 244 AA.
 XX
 AC AAU78286;
 DT 18-JUN-2002 (first entry)
 DE Human TRANCE protein splice variant 2.
 XX
 KW Human: tumour necrosis factor-related activation induced cytokine;
 KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
 KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
 KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
 KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
 KW cartilage growth; skeletal growth.
 XX
 OS Homo sapiens.
 PN WO200216551-A2.
 PD 28-FEB-2002.
 XX
 PF 20-AUG-2001; 2001WO-US26101.
 PR 15-APR-1997; 97JP-0097808.
 PR 18-AUG-2000; 2000US-226197P.

XX
 XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
 PA
 PI Choi Y, Odgren PR, Marks SC;
 XX
 DR WPI: 2002-304119/34.
 DR N-PSDB; ABR12877.
 XX
 PT Treating mammal having disorder characterised by abnormal
 PT cartilage/skeletal growth such as dwarfism, acromegaly, by
 PT administering tumour necrosis factor-related activation induced
 PT cytokine-modulating agent to mammal -
 XX
 PS Disclosure; Fig 4; 55pp; English.
 XX
 CC The present invention relates to a new method of treating a mammal
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth. The method of the invention involves administering to
 CC the mammal a tumour necrosis factor-related activation induced cytokine
 CC (TRANCE)-modulating agent. The method is useful for treating a mammal
 CC having a disorder comprising insufficient or excessive cartilage or
 CC skeletal growth, where the disorder comprising insufficient cartilage or
 CC skeletal growth is selected from dwarfism, osteopetrosis,
 CC craniofacial-skeletal discrepancies and bone or cartilage damage
 CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
 CC arthritis, and disorders comprising excessive cartilage or skeletal
 CC growth are selected from acromegaly, gigantism, exostosis, cartilage,
 CC exostosis bursata and multiple osteocartilaginous exostoses. The method
 CC is useful for inhibiting chondrocyte differentiation. The present amino
 CC acid sequence represents the human TRANCE protein, splice variant 2, of
 CC the invention. TRANCE is a member of the tumour necrosis factor family
 CC and acts directly on cartilage-producing cells (chondrocytes).
 CC
 SO Sequence 244 AA;
 Query Match 39.7%; Score 180.5; DB 23; Length 244;
 Best Local Similarity 59.7%; Pred. No. 1.5e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 OY 15 IPSISHEAKRTSLSSWKHDQDANVSNMTFSNGKLRV--GIYRRNADICSRHRTVSAGL 72
 DB 102 IPSGS---HKVSLSSWYHDMGNAKISNMTFSNGKLIYNODGFYLVANICFRHHTSGDL 158
 OY 73 TLQDPLQ 79
 DB 159 ATEYLQL 165
 RESULT 7
 AA083020
 ID AA083020 standard; Protein; 246 AA.
 XX
 AC AA083020;
 DT 10-FEB-1999 (first entry)
 DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX
 KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human.
 XX
 OS Homo sapiens.
 PN WO9846644-A1.
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.


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PR 15-APR-1997; 97JP-0097808.
PR 09-JUN-1997; 97JP-0151434.
PR 12-AUG-1997; 97JP-0217897.
PR 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI: 1998-594563/50.
DR N-PSDB; AAV69887.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
PT for, e.g. treatment and investigation of disorders of bone and
PT calcium metabolism
XX
XX Claim 36; Pages 113-114; 151pp; Japanese.
XX
XX The present sequence represents an osteoclastogenesis inhibitory factor
CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC separation and maturation of osteoclasts in the presence of bone
CC absorption factors such as calcitriol or parathyroid hormone (PTH).
CC OBM is isolated from stroma cells cultured in the presence of a bone
CC absorption factor by separation and solubilisation of membrane proteins
CC then affinity chromatography using OCIF. It exists in a full-sequence
CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
CC used for screening potential inhibitors and modifiers of its biological
CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
XX Sequence 317 AA:
SQ
XX
XX Query Match 39.7%; Score 180.5; DB 19; Length 317;
XX Best Local Similarity 59.7%; Pred. No. 2.1e-14;
XX Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
XX
QY 15 IPSISHEAKTSSSWKHDQDANVSNMTPFSGKLRK--GIYYRNADICSRHRTVSAGL 72
DB ||| | ||| ||| | ||| ||| ||| | ||| ||| ||| | ||| ||| ||| |
175 IPSGS---HKVSLSSWYHDSRGWAKISNMTPFSGKLLVNDGFFYLLANICFRHHETSGDL 231
QY 73 TLQDLQL 79
DB : |||
232 ATEYLQL 238
XX
XX RESULT 10
XX AAW69957
XX ID AAW69957 standard; Protein; 317 AA.
XX
XX AAW69957;
XX
XX 08-OCT-1998 (first entry)
XX
XX NF-kB receptor activator RANK ligand (RANKL).
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW Immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9828426-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23775.
XX
XX 14-OCT-1997; 97US-0064671.
XX
XX

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PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX WPI: 1998-377657/32.
DR N-PSDB; AAV41378.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
XX Claim 27; Pages 59-60; 80pp; English.
XX
XX This represents a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.
XX
XX Sequence 317 AA:
SQ
XX
XX Query Match 39.7%; Score 180.5; DB 19; Length 317;
XX Best Local Similarity 59.7%; Pred. No. 2.1e-14;
XX Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
XX
QY 15 IPSISHEAKTSSSWKHDQDANVSNMTPFSGKLRK--GIYYRNADICSRHRTVSAGL 72
DB ||| | ||| ||| | ||| ||| ||| | ||| ||| ||| | ||| ||| ||| |
175 IPSGS---HKVSLSSWYHDSRGWAKISNMTPFSGKLLVNDGFFYLLANICFRHHETSGDL 231
QY 73 TLQDLQL 79
DB : |||
232 ATEYLQL 238
XX
XX RESULT 11
XX AAW68293
XX ID AAW68293 standard; Protein; 317 AA.
XX
XX AAW68293;
XX
XX 08-OCT-1998 (first entry)
XX
XX NF-kB receptor activator RANK ligand (RANKL).
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW Immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9828424-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23866.
XX
XX

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XX 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI: 1998-377655/32.
 DR N-PSDB; AAV41372.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 59-60; 80pp; English.

XX This represents a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 317 AA:

Query Match 39.7%; Score 180.5; DB 19; Length 317;
 Best Local Similarity 59.7%; Pred. No. 2.1e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

OY 15 IPSISHEAKHTSLSSWKHDODANVSNMFTSNGKLRVK--GIYYRNDICSRHRTVTSAGL 72
 Db 175 IPSSG---HKVSLSSWYHGRGAKISNMFTSNGKLIYNODGFYLLANICFRHHTSGDL 231

OY 73 TLQDLQL 79
 : |||
 Db 232 ATEYLQL 238

RESULT 12
 AAY84417
 ID AAY84417 standard; Protein; 317 AA.

AC AAY84417;

DT 25-JUL-2000 (first entry)

XX Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.

OS Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 49..69
 FT Domain 70..157
 FT Region 158..317

FT /note= "extracellular stalk domain"
 FT /note= "active ligand moiety"

XX WO200015807-A1.

XX 23-MAR-2000.

XX 13-SEP-1999; 99WO-DK00481.

XX 15-SEP-1998; 98DK-0001164.

XX 02-OCT-1998; 98US-0102896.

XX (MEBT-) M & E BIOTECH AS.

XX Halkier T, Haaning J;

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -

XX WPI: 2000-271444/23.
 DR N-PSDB; AA299964.

XX Claim 19; Page 78-79; 110pp; English.

XX The present sequence represents a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 317 AA:

Query Match 39.7%; Score 180.5; DB 21; Length 317;
 Best Local Similarity 59.7%; Pred. No. 2.1e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;

OY 15 IPSISHEAKHTSLSSWKHDODANVSNMFTSNGKLRVK--GIYYRNDICSRHRTVTSAGL 72
 Db 175 IPSSG---HKVSLSSWYHGRGAKISNMFTSNGKLIYNODGFYLLANICFRHHTSGDL 231

OY 73 TLQDLQL 79
 : |||
 Db 232 ATEYLQL 238

RESULT 13
 AAE08738
 ID AAE08738 standard; Protein; 317 AA.

AC AAE08738;

DT 15-NOV-2001 (first entry)

XX Human receptor activator of NF kappaB ligand (RANKL) protein.

XX Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

OS Homo sapiens.

XX US6271349-B1.

XX 07-AUG-2001.

XX 17-DEC-1998; 98US-0215649.
 PF 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0772330.
 PR 07-MAR-1997; 97US-0813509.
 PR 22-DEC-1997; 97US-0996139.
 XX (IMMUNEX CORP.
 PA Dougall WC, Galibert L;
 PI MPI: 2001-520313/57.
 DR N-PSDB: AAD15311.
 XX
 PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for
 PT regulating immune response, in screening for RANK inhibitors, or as an
 PT adjunct therapy for disease characterized by neoplastic cells that
 PT express RANK -
 PS
 XX Example 15; Column 71-72; 47pp; English.
 CC The patent discloses novel receptor activator of nuclear factor (NF)-
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
 CC of the tumor necrosis factor (TNF) receptor superfamily and associates
 CC with TNF receptor associated factor (TRAF) 2 and 3 which are important
 CC in the regulation of immune and inflammatory response. The receptors
 CC are useful for regulating immune response and in screening for inhibitors
 CC of these receptors. The cytoplasmic domain of RANK is used in developing
 CC assays for inhibitors of signal transduction, e.g. for screening the
 CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
 CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
 CC are useful in ameliorating the negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, acute inflammatory
 CC reactions and the effects of bone resorption. RANK acts as an anti-
 CC apoptotic signal and rescue the cells that express RANK from apoptosis.
 CC Soluble forms of the receptor are used in vivo or in vitro based
 CC screening tests for agonists or antagonists of RANK activity, as
 CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit
 CC transduction of a signal via RANK. RANK compositions are used in the
 CC development of both agonistic and antagonistic antibodies, or as an
 CC adjunct therapy for disease characterized by neoplastic cells that
 CC express RANK. Compounds that interfere with RANK/TRAF6 interactions
 CC are useful for modulating the formation of osteoclasts from osteoclast
 CC precursors and for modulating osteoclast function and activities. They
 CC are used as inhibitors of diseases associated with excess bone resorption
 CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
 CC useful for the expression of recombinant proteins, as probes for analysis
 CC of the presence or distribution of RANK transcripts, while the proteins
 CC are useful in preparing kits for the detection of soluble RANK, or
 CC monitor RANK-related activity. The present sequence is RANK ligand
 CC (RANKL) protein from human.
 CC
 XX
 SQ Sequence 317 AA:
 Query Match 39.7%; Score 180.5; DB 22; Length 317;
 Best Local Similarity 59.7%; Pred. No. 2,1e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 QY 15 IPSISHEAKTSLSSWKHDQDQWVSNMTFSNGKLRVK--GIYRNADICSRHRYTSAGL 72
 Db 175 IPSGS---HKVSLSSWYHDKGAKISNMTFSNGKLIYVODGFYLYANICFRHHTSGDL 231
 QY 73 TLQDLQL 79
 Db 232 ATEYLQL 238
 RESULT 14
 AAE04426

ID AAE04426 standard; Protein; 317 AA.
 XX
 AC AAE04426;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human receptor activator of NF-chi B ligand (huRANKL) protein.
 XX
 KW Human: receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF;
 KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
 KW Chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 162..317
 FT /note="Receptor binding region"
 XX
 XX US6242213-B1.
 PD 05-JUN-2001.
 XX
 PF 22-DEC-1997; 97US-0995659.
 XX
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 XX
 PA (IMMUNEX CORP.
 PI Anderson DM;
 XX
 DR MPI: 2001-407216/43.
 DR N-PSDB: AAD06715.
 XX
 PT New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF-chi B
 PT receptor activator) of the receptor activator of NF-chi B (RANK) -
 XX
 PS Claim 1; Column 65-66; 43pp; English.
 XX
 CC The present invention relates to receptor activator of NF-chi B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumor necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
 CC The ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
 CC protein.
 CC
 XX
 SQ Sequence 317 AA:
 Query Match 39.7%; Score 180.5; DB 22; Length 317;
 Best Local Similarity 59.7%; Pred. No. 2,1e-14;
 Matches 40; Conservative 4; Mismatches 18; Indels 5; Gaps 2;
 QY 15 IPSISHEAKTSLSSWKHDQDQWVSNMTFSNGKLRVK--GIYRNADICSRHRYTSAGL 72
 Db 175 IPSGS---HKVSLSSWYHDKGAKISNMTFSNGKLIYVODGFYLYANICFRHHTSGDL 231
 QY 73 TLQDLQL 79
 Db 232 ATEYLQL 238
 RESULT 15
 AAE01993
 ID AAE01993 standard; Protein; 317 AA.
 XX
 AC AAE01993;
 XX

DT 31-JUL-2001 (first entry)

DE Human full-length RANKL (receptor activator of NF-kappaB ligand).

XX
XX
KW Human: receptor activator of NF-kappaB: RANK: nuclear factor-kappaB:
NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
inflammatory reaction; bone resorption; gene therapy; immunomodulator;
immune system dysfunction; familial expansile osteolysis; FEO;
early onset Paget's disease of bone; EP; cystostatic; chromosome 13q14.

XX Homo sapiens.

XX WO200136637-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-US31459.

XX 17-NOV-1999; 99US-0442029.

XX (IMMUNEX) IMMUNEX CORP.

XX PI Anderson DM, Hughes AE;

XX WPI; 2001-329222/34.

DR N-PSDB; AAD05904.

XX
XX
PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
PS Disclosure; Page 76-77; 96pp; English.

XX
CC The present invention relates to a novel receptor, referred to as RANK
CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a type I
CC transmembrane protein that interacts with TNF receptor-associated
CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
CC of the transcription factor NF-kappaB, a ubiquitous transcription factor
CC that is most extensively utilised in cells of the immune system.
CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
CC negative effects of inflammatory reactions, and the effects of excess
CC bone resorption. The RANK DNAs, proteins and their analogues are useful
CC for the preparation of pharmaceutical compositions, for infecting target
CC cells for use in gene therapy applications in diagnosing diseases
CC associated with RANK, and as targets for use in screening assays. They
CC may be used in the treatment or diagnosis of immune system dysfunction.
CC The present invention also encompasses gene therapy methods to correct
CC gene-activating mutations, associated with e.g. familial expansile
CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC present amino acid sequence is full-length human RANKL (huRANKL)
CC protein. The RANKL gene is located in chromosome 13q14.

XX
SQ Sequence 317 AA;

Query Match 39.7%; Score 180.5; DB 22; Length 317;

Best Local Similarity 59.7%; Pred. No. 2.1e-14; Mismatches 2;

Matches 40; Conservative 4; Indels 5; Gaps 2;
OY 15 IPSISHAHKTSLSKWHDQMANVSNMFTSNGKLRVYK--GIYYRNADICSRHRTSAGL 72
DB 175 IPSGS---HKVSLSSMYHBRGMAKISMFTSNGKLIYNQDGFYLYANICFRHHTSGDL 231
OY 73 TLQDLQL 79
DB 232 ATEYIQL 238

Search completed: December 8, 2002, 19:30:31
Job time : 56.2613 secs

1
2
3

Tue Dec 10 10:51:38 2002

us-09-880-457-1_copy_543_746.rst

Page 1

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:16:58 ; Search time 450.782 Seconds
(without alignments)
7329.213 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthm:*
3: em_estlu:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.6	46.4	659	17	AG107545
2	84	41.2	612	17	BH267783
3	46.2	22.6	362	10	AV653073
4	33.8	16.5	284	17	AL768846
5	33.6	16.3	530	9	AA310614
6	33.2	16.3	853	17	BH314331

7	32.8	16.1	407	10	AW750032	AW750032	PM2-BT054
8	32.8	16.1	561	10	AV979271	AV979271	AV979271
9	32.8	16.1	724	17	BH617165	BH617165	BH617165
10	32.4	15.9	823	17	CNS05974	CNS05974	CNS05974
11	32.4	15.9	1027	14	BQ050697	BQ050697	BQ050697
12	32.2	15.8	771	17	A2724950	A2724950	A2724950
13	32	15.7	463	12	BF930674	BF930674	BF930674
14	32	15.7	912	12	BF683775	BF683775	BF683775
15	31.8	15.6	428	9	AU226504	AU226504	AU226504
16	31.6	15.5	426	17	AQ523546	AQ523546	AQ523546
17	31.6	15.5	451	13	BU445420	BU445420	BU445420
18	31.4	15.4	341	10	AW784685	AW784685	AW784685
19	31.4	15.4	1074	9	A1896022	A1896022	A1896022
20	31.4	15.4	1074	17	CNS04422F	CNS04422F	CNS04422F
21	31.2	15.3	306	9	AA188893	AA188893	AA188893
22	31.2	15.3	483	10	AW750034	AW750034	AW750034
23	31.2	15.3	493	10	AW959012	AW959012	AW959012
24	31.2	15.3	517	10	AW959012	AW959012	AW959012
25	31.2	15.3	545	13	B1260179	B1260179	B1260179
26	31.2	15.3	558	14	BM836932	BM836932	BM836932
27	31.2	15.3	646	10	AW958677	AW958677	AW958677
28	31.2	15.3	694	10	AW814742	AW814742	AW814742
29	31.2	15.3	698	17	AC013309	AC013309	AC013309
30	31.2	15.3	701	12	BG768911	BG768911	BG768911
31	31.2	15.3	728	12	BG761703	BG761703	BG761703
32	31.2	15.3	729	12	BG422303	BG422303	BG422303
33	31.2	15.3	743	12	BG284886	BG284886	BG284886
34	31.2	15.3	792	13	BM044745	BM044745	BM044745
35	31.2	15.3	819	17	BH419036	BH419036	BH419036
36	31.2	15.3	836	17	BH505193	BH505193	BH505193
37	31.2	15.3	844	14	BQ895831	BQ895831	BQ895831
38	31.2	15.3	847	14	BQ900660	BQ900660	BQ900660
39	31.2	15.3	871	14	BQ935750	BQ935750	BQ935750
40	31.2	15.3	907	14	BQ220873	BQ220873	BQ220873
41	31.2	15.3	910	14	BQ918817	BQ918817	BQ918817
42	31.2	15.3	916	10	BE542870	BE542870	BE542870
43	31.2	15.3	941	12	BE782157	BE782157	BE782157
44	31.2	15.3	959	14	BQ894167	BQ894167	BQ894167
45	31.2	15.3	974	14	BQ053094	BQ053094	BQ053094

ALIGNMENTS

RESULT 1
AG107545
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-112609.F, genomic survey sequence.
ACCESSION
AG107545
VERSION
AG107545.1 GI:16728063
KEYWORDS
GSS.
ORGANISM
Pan troglodytes male lymphoblast DNA, clone: PTB Chimpanzee Male
BAC Library clone: PTB-112609.F.
REFERENCE
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chiampesgsc.riken.go.jp, URL: http://hnp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.

PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pRS145
R Site 1 : SacI
R Site 2 : SacI
Location/Qualifiers
1. .659
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PMB-112609.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 181 a 168 c 121 g 189 t
ORIGIN

Query Match
Best Local Similarity 46.4%; Score 94.6; DB 17; Length 659;
Matches 134; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

QY 8 CTCATTAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGTCCTCCACA 67
Db 410 CCCATTAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGTCCTCCACA 67
QY 68 TGACTTTGACGACGGAAGAACTAAGAGTCA-----AAGCATTTATTAACCGGAATGCCG 121
Db 470 TGACTTTGACGACGGAAGAACTAAGAGTCA-----AAGCATTTATTAACCGGAATGCCG 121
QY 122 ACATTGGCTCTGACATCGGCTAAGCTCAGAGGCTTACCTGCGAGGACCTTCAGCTA 180
Db 530 ACATTGGCTCTGACATCGGCTAAGCTCAGAGGCTTACCTGCGAGGACCTTCAGCTA 180

RESULT 2
BH267783/c 612 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-186C1.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
LOCUS BH267783
ACCESSION CH230-186C1, DNA sequence.
VERSION BH267783
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorjais, E., Overton, U., Russell, D., Chen, D., Rlygs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcorI segment
Unpublished (1999)
Other: GSS: CH230-186C1.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

TITLE
JOURNAL
COMMENT
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@tigr.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orcinfo/infomation.htm). BAC end
plate: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .612
/organism="Rattus norvegicus"

FEATURES

source
1. .612
/organism="Rattus norvegicus"

/strain="BN/SSNhsd/MCw"
/db_xref="taxon:10116"
/clone="CH230-186C1"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site 1: EcorI; Site 2: EcorI;
CHORI-230 Rat (BN/SSNhsd/MCw) BAC library produced by
Pieter de Jong"

BASE COUNT 168 a 145 c 133 g 166 t
ORIGIN

Query Match
Best Local Similarity 41.2%; Score 84; DB 17; Length 612;
Matches 127; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

QY 8 CTCATTAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGTCCTCCACA 67
Db 591 CCCATTAAGAGCTCTTCTTCTTGAAACATGACCAAGATTGGGCAACGTCCTCCACA 67
QY 68 TGACTTTGACGACGGAAGAACTAAGAGTCA-----AAGCATTTATTAACCGGAATGCCG 121
Db 531 TGACTTTGACGACGGAAGAACTAAGAGTCA-----AAGCATTTATTAACCGGAATGCCG 121
QY 122 ACATTGGCTCTGACATCGGCTAAGCTCAGAGGCTTACCTGCGAGGACCTTCAGCTA 179
Db 471 ACATTGGCTCTGACATCGGCTAAGCTCAGAGGCTTACCTGCGAGGACCTTCAGCTA 179

RESULT 3
AV653073 362 bp mRNA linear EST 15-JAN-2002
DEFINITION AV653073 GLC Homo sapiens cDNA clone GLCDB01.3, mRNA sequence.
LOCUS AV653073
ACCESSION AV653073
VERSION AV653073.1 GI:9874087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 362)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Gu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. .362
Location/Qualifiers
1. .362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCDB01"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site 1: EcorI; Site 2:
XhoI"

BASE COUNT 102 a 80 c 78 g 100 t 2 others
ORIGIN

Query Match

22.6%; Score 46.2; DB 10; Length 362;

OY 71 CTTGACGACGAGAACTAGATCAAGGCAATTTATACGGATGCGGACATT 126
 Db 345 NTTNAATGTGGGACAGGACATTCATTAAGCATTTATGTGAATNGCAGAAATT 400

RESULT 6 BH314331 LOCUS

DEFINITION BH314331 853 bp DNA linear GSS 03-DEC-2001
 CH230-99C2.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
 BH314331
 VERSION BH314331
 KEYWORDS GSS.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE AUTHORS

1 (bases 1 to 853)
 Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
 A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
 Jong, P. and Fraser, C. M.
 Rat BAC End Sequences from Library CHORI-230 EcORI segment.
 JOURNAL Unpublished (1999)
 COMMENT Other-GSS: CH230-99C2.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@tigr.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ordering information.htm). BAC end
 plates: 99 row: C column: 2
 Seq primer: 77
 Class: BAC ends.
 FEATURES
 source Location/Qualifiers
 1..853
 /organism="Rattus norvegicus"
 /strain="BN/SSNhsd/MCM"
 /db_xref="taxon:10116"
 /clone="CH230-99C2"
 /clone_lib="CHORI-230 Segment 1"
 /sex="Female"
 /cell_type="Brain"
 /note="Vector: pTARBAC2.1; Site_1: EcORI; Site_2: EcORI;
 CHORI-230 Rat (BN/SSNhsd/MCM) BAC library produced by
 Pieter de Jong"

BASE COUNT 302 a 190 c 184 g 177 t
 ORIGIN

Query Match 16.3%; Score 33.2; DB 17; Length 853;
 Best Local Similarity 53.0%; Pred. No. 1.8;
 Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

OY 2 ATGAGGCTCAATAAAGCGCTTCTTCTTGGAAACATGACCAAGATTGGCAACGCT 61
 Db 430 ATGAAATTCATAGCAAAATGTTGGACTGGAAGAAACATCATCTGAGAGCTAACCAT 489
 OY 62 CCAACATGACTTTCGACGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 121
 Db 490 CCAAGAGACATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121
 OY 122 ACATTTCTCTCGA 135
 Db 550 TGAATTAATCTAGA 563

RESULT 7
 AW750032 407 bp mRNA linear EST 28-APR-2000
 PM2-BT0546-120100-001-a08 BT0546 Homo sapiens cDNA, mRNA sequence.
 LOCUS AW750032
 DEFINITION AW750032.1 GI:7664964
 VERSION AW750032.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 407)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
 Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,
 M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-BT0546-
 120100-001-a08&t3=2000-01-12&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 406.
 FEATURES
 source Location/Qualifiers
 1..407
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BT0546"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from OHSR185 PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 135 a 73 c 109 g 90 t
 ORIGIN

Query Match 16.1%; Score 32.8; DB 10; Length 407;
 Best Local Similarity 55.2%; Pred. No. 1.7;
 Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

OY 11 ATAAACGAGCTTCTTCTTGGAAACATGACCAAGATTGGCAACGCTCCAAACATGA 70
 Db 258 AAACAACGAGCCAAAGCTCCAGAAATGCTGCCAAGCTGGAAGAGAGTTGAAGCAGCA 317
 OY 71 CTTGACGACGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 126
 Db 318 ATGAAATGTGGGACAGGACAGGACATTCATTAAGCAATGAGGACAGACATT 373

RESULT 8
 AV979271 561 bp mRNA linear EST 14-MAR-2002
 DEFINITION AV979271 Nori Satoh unpublished cDNA library, egg clona
 intestinalis cDNA clone cleg52120 5', mRNA sequence.
 ACCESSION AV979271
 VERSION AV979271.1 GI:19468995
 KEYWORDS EST.

BASE COUNT	226	a	1226	g	192	t
ORIGIN						
Query Match	16.1%	Score 32.8;	DB 17;	Length 724;		
Best Local Similarity	50.0%	Pred. No. 2,3;				
Matches	82;	Conservative	0;	Mismatches	82;	Indels
					0;	Gaps
						0;
OY	1	CATGAGGCTCATAAACGAGCTCTTCTTCTTGGAAACATACCAACATTTGGGCAACGNC	60			
Db	688	CAAGATGAAAGATTAATGGAAGATGTCGAAACCTTAACCTACTGAAGATTGAGAAATCTTC	629			
OY	61	TCCACATGACTTTTCAGCAACGCAAACTAAGCTCAAGGCAATTTATTCGGAATGCC	120			
Db	628	TAAATCAATTAATGAGCAAGAAATCATCTACTACGAAAGAAAGGTTTCATTTTCTCC	569			
OY	121	GACATTTGCTCTCGACATCGCGTAACCTCAGCAGGCTTAACCTC	164			
Db	568	AAGCTTTGGTGCGCTTCTCTCTCCTGGAAGTCGCGCTCTCTC	525			
RESULT 10						
CNS05RMX/C	823 bp		DNA	linear	GSS 26-MAY-2000	
LOCUS	Tetradon nigroviridis genome survey sequence Sp6 end of clone					
DEFINITION	004K23 of library B from Tetradon nigroviridis, genomic survey sequence.					
ACCESSION	AL350754.1 GI:8244524					
VERSION	AL350754.1					
KEYWORDS	GSS; genome survey sequence.					
SOURCE	Tetradon nigroviridis.					
ORGANISM	Tetradon nigroviridis					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradon.					
REFERENCE	1 (bases 1 to 823)					
AUTHORS	Roest-Collins,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brothier,P., Quetier,F., Saurin,W. and Weissenbach,J.					
TITLE	Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 823)					
AUTHORS	Roest-Collins,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.					
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis					
JOURNAL	Unpublished					
REFERENCE	3 (bases 1 to 823)					
AUTHORS	Genoscope.					
TITLE	Direct Submission					
JOURNAL	Submitted (12-APR-2000)					
COMMENT	This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetradon .					
FEATURES	Location/Qualifiers					
source	1..823					
	/organism="Tetradon nigroviridis"					
	/db_xref="taxon:99883"					
	/clone="004K23"					
	/clone_1fb="B"					
	/note="Genoscope sequence ID : COAB004FF12B1-end : Sp6"					
BASE COUNT	185	a	154	c	189	g
ORIGIN	259 t 36 others					

Query Match 15.9%; Score 32.4; DB 17; Length 823;
 Best Local Similarity 50.4%; Pred. No. 3.3;
 Matches 63; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

OY 71 CTTTACGACGACGAACTAAGATCAAGGCAATTTATTACCGAATGCCGACATTTGCT 130
 DB 731 CTTTGCNCAAAAANANATTAACCAANTTAACCTTTTNCACCCCAACGCCAGCTCAGCG 672
 OY 131 CTCGACATCGCGTACACCGAGCGCCCTACCTGACGACCTTCACTATGCTGTAATT 190
 DB 671 CTTGACACCGTGGAGNTGAGAACACACACACACACACACACACACACACACAC 612
 OY 191 TGACA 195
 DB 611 TGANA 607

RESULT 11
 B0050697/c 1027 bp mRNA linear EST 29-MAR-2002
 LOCUS AGENCOURT_6808690 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784700
 DEFINITION 5', mRNA sequence.
 ACCESSION B0050697
 VERSION B0050697.1 GI:19810037
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1027)
 NIH-MGC http://mgi.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: AFCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://llnl.gov
 Plate: LLM12870 row: k column: 05
 High quality sequence stop: 642.

FEATURES
 source Location/Qualifiers
 1..1027

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5784700"
 /clone_lib="NIH_MGC_71"
 /tissue_type="telomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb.
 BASE COUNT 286 a 233 c 214 g 292 t 2 others
 ORIGIN

Query Match 15.9%; Score 32.4; DB 14; Length 1027;
 Best Local Similarity 53.7%; Pred. No. 3.7;
 Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

OY 9 TCATAAAGCGATCTTCTTCTTGAAGACATGACCAAGATTGGGCAACGCTCCACAT 68
 DB 688 TCAAAATTAAGTTTATTTTGAAGAACTGTATTAACCTTGGAAACAAGTNTAAACA 629
 OY 69 GACTTTCAGCAACGAAACTAAGATCAAGGCAATTTATTACCGAATGCCGACATTTG 128
 DB 628 TTTTATTAGTTGGAAAGTAATCTGAAGAAGTAATATTCAATTAATCAATCAATCAG 569
 OY 129 CTC 131
 DB 568 CTC 566

RESULT 12
 A2724950 771 bp DNA linear GSS 24-JAN-2001
 LOCUS RPCI-24-64B19.TJ RPCI-24 Mus musculus genomic clone RPCI-24-64B19,
 DNA sequence.

ACCESSION A2724950
 VERSION A2724950.1 GI:12471113
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 771)
 Zhao S., Nierman W., Malek J., Shatsman S., Akintet B., Levins M.,
 Tsegaye G., Geer K., Krol M., Shvartsbeyn A., Gebregorgis E.,
 Russell D., de Jong P. and Fraser C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 COMMENT Other GSSs: RPCI-24-64B19.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPC
 Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
 plate: 64 row: B column: 19
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..771

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-64B19"
 /clone_lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTRABAC1; Site_1: BamHI; Site_2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTRABAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."
 BASE COUNT 331 a 110 c 131 g 199 t
 ORIGIN

Query Match 15.8%; Score 32.2; DB 17; Length 771;
 Best Local Similarity 52.6%; Pred. No. 3.8;
 Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

OY 28 TCTTGAAGACATGACCAAGATTGGGCAACGCTCCACATGACTTTCAGCAACGGAAGA 87
 DB 199 TTTTGAAGATTAAGAAAGATTGACAAATCTCCAGCAACATCAACAGGGAAGAAAG 258
 OY 88 CTAAAGCTCAAGGATTTATTACCGGAATGCCGACATTTGCTTCGACATCGCTAAC 147
 DB 259 ATCCAAATCAATACGCTTATGATCAAAAGAGAGCCATTAATATATTCAGGAATTC 318
 OY 148 TCAGCAGGCTTAA 160
 DB 319 AGTCAGGCTTAA 331

RESULT 13
 BF930674 463 bp mRNA linear EST 22-JAN-2001
 LOCUS BF930674

[illegible]

REFERENCE	1 (bases 1 to 912)	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LICM1161 row: c column: 16 High quality sequence stop: 720.	
FEATURES	Location/Qualifiers	
source	1..912 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4301127" /clone_lib="NIH.MGC.46" /issue_type="leiomysarcoma cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: uterus; Vector: pOT57; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."	
BASE COUNT	295 a 181 c 258 g 178 t	
ORIGIN		
Query Match	15.7%; Score 32; DB 12; Length 912;	
Best Local Similarity	50.0%; Freq. No. 4.8;	
Matches	80; Conservative 0; Mismatches 80; Indels 0; Gaps 0;	
QY	11 ATAAACGAGTCTTCTCTCTTGGAAACATGACAGATGGGCAAAAGCTCCACATGA 70	
Db	361 AAACACGACGACCACTCCAGAAATGCTGCCCAAGCTGAGAAAGATTGAAGCAGCA 420	
QY	71 CTTTCAGCAGCGAAACTAGAGTCMAAGCAATTATTACCGGAATGCCGCAATTGCT 130	
Db	421 ATTGATTGTGGGAACAGGAAACATTCMAAGCAATTTATGTGTAATGGCAGAAATTCATG 480	
QY	131 CTCGACATGCGCGTAACCTCAGCAGGCGCTAACCTCTGGAGCA 170	
Db	481 GAGTATGTGGCAAGCAATGGAGATGCATGCATGGAGAA 520	
RESULT 15		
LOCUS	AU226504 428 bp RNA linear EST 23-APR-2002	
DEFINITION	AU226504 RAF1L4 Arabidopsis thaliana cDNA clone RAF1L4-39-G24 3',	
ACCESSION	AU226504	
VERSION	AU226504.1 GI:19741151	
KEYWORDS	EST.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS	Rossmatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
	ROSIDS: eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
	1 (bases 1 to 428)	
	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,	
	Akiyama,K., Ejiri,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,	
	Itoh,M., Ishii,Y., Areakawa,T., Shibata,K., Shimagawa,A., Muramatsu	
	,M., Hayashizaki,Y. and Shinozaki,K.	
TITLE	Large scale analysis of Arabidopsis full-length cDNA	
JOURNAL	Unpublished (2002)	

COMMENT

Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@tc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLX-1 vector (Carinci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified Bluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source

Location/Qualifiers

1..428
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL14-39-G24"
/clone_lib="RAFL14"
/tissue_type="root"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI"

BASE COUNT 140 a 92 c 73 g 123 t
ORIGIN

Query Match 15.6%; Score 31.8; DB 9; Length 428;
Best Local Similarity 54.8%; Pred. No. 4;

Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 15 AACGAGCTCTTCTTGGAAACATGACCAAGATTGGCAACGCTCCACATGACTTT 74
||| ||||| ||| || | | | || || || ||
DB 16 AATGTTCTTCTTAATTAATCAACATCATCATGACATGACAAACAAAGTGTGATT 75
||| ||||| ||| || | | | || || || ||
QY 75 CAGCAACGAAACTAAGAGCTCAAGGCAATTATTACCGGAATGCCGACATTTC 129
||| || | | || |||| |||| | |||| | | || || ||
DB 76 CAGAGAGAAATATCTCAGAGTTTAAGAGAAATATTACTCATTACGATTGTTTC 130
||| || | | || |||| |||| | |||| | | || || ||

Search completed: December 8, 2002, 19:27:16
Job time : 459.782 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:14 ; Search time 58.0886 Seconds
(without alignments)
7908.746 Million cell updates/sec

Title: US-09-880-457-1_COPY_543_746

Perfect score: 204
Sequence: 1 catgagcctcataaacgag.....gtatttgagatcattcac 204

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	95.1	1186	24	ABK33576
2	96.4	47.3	741	19	AAV69889
3	96.4	47.3	954	19	AAV69887
4	96.4	47.3	954	19	AAV1378
5	96.4	47.3	954	19	AAV1372
6	96.4	47.3	954	22	AAV15311
7	96.4	47.3	954	22	AAV08715
8	96.4	47.3	954	22	AAV05904
9	96.4	47.3	1945	24	ABK12877

10	96.4	47.3	2226	24	ABK12876
11	96.4	47.3	2271	21	AAZ99964
12	96.4	47.3	2274	19	AAV70285
13	96.4	47.3	2390	24	ABK40274
14	93.2	45.7	1823	20	AAV80223
15	84	41.2	957	22	AAV68481
16	80.8	39.6	735	19	AAV69898
17	80.8	39.6	951	21	AAV69900
18	80.8	39.6	951	21	AAV39156
19	80.8	39.6	951	21	AAZ99965
20	80.8	39.6	951	21	AAZ99965
21	80.8	39.6	1538	21	AAZ99965
22	80.8	39.6	1574	22	AAH25526
23	80.8	39.6	1630	19	AAV41377
24	80.8	39.6	1630	19	AAV41371
25	80.8	39.6	1630	22	AAV15310
26	80.8	39.6	1630	22	AAV08714
27	80.8	39.6	1630	22	AAV08714
28	80.8	39.6	2029	21	AAV39155
29	80.8	39.6	2191	19	AAV41489
30	80.8	39.6	2237	20	AAV80224
31	80.8	39.6	2237	24	ABK12880
32	80.8	39.6	2295	19	AAV70284
33	80.8	39.6	2295	21	AAZ99966
34	79.2	38.8	519	21	AAZ99968
35	61.8	30.3	519	21	AAZ99969
36	61.8	30.3	519	21	AAZ99972
37	61.8	30.3	546	21	AAZ99971
38	61.8	30.3	564	21	AAZ99970
39	61.8	30.3	564	21	AAZ99970
40	61.8	25.1	519	21	AAZ99973
41	51.2	15.3	519	20	AAV87615
42	31.2	15.3	985	24	ABK46140
43	31.2	15.3	2276	22	ABA08774
44	31.2	15.3	3073	24	ABK46139

ALIGNMENTS

RESULT 1
ABK33576
ID ABK33576 standard; cDNA; 1186 BP.
AC ABK33576;
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 81.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220648P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.

cDNA encoding huma
DNA encoding a hum
Human osteoprotege
cDNA encoding huma
Human TRANCE encod
Krat osteoclast dif
Nucleic acid encod
Nucleotide sequenc
Mouse OBM nucleoti
DNA encoding a mur
Osteoclast formati
Nucleic acid encod
Nucleotide sequenc
NF-KB receptor act
NF-KB receptor act
Murine receptor ac
Murine receptor ac
Mouse RANKL (rece
Mouse OBM nucleoti
Nucleotide sequenc
Murine TRANCE enco
cDNA encoding mous
Human osteoprotege
DNA encoding a mur
Mouse cDNA encodin
DNA encoding a syn
DNA encoding a mur
DNA encoding osteo
DNA encoding osteo
DNA encoding osteo
DNA encoding osteo
EST clone D611.
cDNA encoding colo
Human cytokinesis
cDNA encoding colo

PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.

PA (GETH) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 DR WPI; 2002-172001/22.
 DR P-SDB; AAU83632.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 XX tumour or liver tumour -
 PS Claim 2; Figure 81; 359pp; English.

CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression in, pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for stimulating
 CC the release of tumour necrosis factor- α from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
 CC PRO protein coding sequences of the invention.

SQ Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;

Query Match 95.1%; Score 194; DB 24; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 2e-57;

Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGAGCTCATTAACGAGTCTTCTTGTGAAACATGACCAAGATTGGCAACGTC 60
 DB 504 CATGAGCTCATTAACGAGTCTTCTTGTGAAACATGACCAAGATTGGCAACGTC 563
 QY 61 TCCACATACCTTTCAGCAACGAAACTAAGAGTCAAGGATTTATACCGGATGCC 120
 DB 564 TCCACATACCTTTCAGCAACGAAACTAAGAGTCAAGGATTTATACCGGATGCC 623
 QY 121 GACATTTGCTCGACATCGGCTAAGCTCAGAGGCTTAAGTTCAGAGCTTCAGCTA 180
 DB 624 GACATTTGCTCGACATCGGCTAAGCTCAGAGGCTTAAGTTCAGAGCTTCAGCTA 180
 QY 181 TGGTGTATTTGAG 194
 DB 684 TGGTGTATTTGAG 697

RESULT 2
 AA69899

XX AAV69899 standard; cDNA to mRNA; 741 BP.
 AC AAV69899;

XX 10-FEB-1999 (first entry)
 DT Nucleic acid encoding a human OCIF-binding molecule (OBM).
 XX
 DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 XX osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.
 XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 1..741

XX /*tag= a

XX WO9846644-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-JP01728.

XX 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 DR WPI; 1998-594563/50.
 DR P-SDB; AAW83020.

XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism

PS Example 28; Pages 121-122; 151pp; Japanese.

CC The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC absorption and maturation of osteoclasts in the presence of bone
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modulators of its biological
 CC function and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC components of drugs.

SQ Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;

Query Match 47.3%; Score 96.4; DB 19; Length 741;
 Best Local Similarity 74.5%; Pred. No. 2e-23;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATTAACGAGTCTTCTTGTGAAACATGACCAAGATTGGCAACGTC 62
 DB 318 TGAGGCTCATTAACGAGTCTTCTTGTGAAACATGACCAAGATTGGCAACGTC 377
 QY 63 CAACATGACTTTCAGCAACGAAACTAAGAGTCA-----AAGCATTTATTCAGGAA 116
 DB 378 CAACATGACTTTCAGCAACGAAACTAAGAGTCA-----AAGCATTTATTCAGGAA 116
 QY 117 TCCGACATTTGCTCGACATCGGCTAAGCTCAGAGGCTTAAGTTCAGAGCTTCAGCTA 176
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 438 TGCCACATTTGCTTCGACATCATGAACTTCAGAGACCTAGCTACAGATATCTTCA 497
 QY 177 GCTA 180
 111
 Db 498 ACTA 501

RESULT 3

AAV69887
 ID AAV69887 standard; cDNA to mRNA; 954 BP.

AC AAV69887;

DE 10-FEB-1999 (first entry)

XX Nucleic acid encoding a human OCIF-binding molecule (OBM).

XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 1..954

XX CDS /tag= a

XX MO9846644-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-JP01728.

XX 02-DEC-1997; 97JP-0332241.

XX 15-APR-1997; 97JP-0097808.

XX 09-JUN-1997; 97JP-015134.

XX 12-AUG-1997; 97JP-0217897.

XX 21-AUG-1997; 97JP-0224803.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;

XX WPI: 1998-594563/50.

XX P-PSDB: AAW63018.

XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism

XX Claim 38; Page 115; 151pp; Japanese.

XX The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stromal cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.

XX Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;

XX Query Match

XX Best Local Similarity

47.3%; Score 96.4; DB 19; Length 954;
 74.5%; Pred. No. 2.3e-23;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATTAAGAGAGCTTCTTCTTGGAAACATGACCAAGTTGGGCAAGCTC 62

Db 531 TGGTTCCTCAATTAAGTAGCTCTCTCTGGTACCATGATGGGGTGGCCAAATCTC 590

QY 63 CAACATGACTTTCAGACACGAAAGTAAGTCA-----AAGCATTTATTTACCGGAA 116

Db 591 CAACATGACTTTCAGACAAAGTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 650

QY 117 TGCCACATTTGCTTCGACATCATGCGTAACCTGACGAGCCCTTACTCTGACGACTTCA 176

Db 651 TGCCACATTTGCTTCGACATCATGCGTAACCTGACGAGCCCTTACTCTGACGACTTCA 710

QY 177 GCTA 180

Db 711 ACTA 714

RESULT 4

AAV41378
 ID AAV41378 standard; cDNA; 954 BP.

AC AAV41378;

DE 08-OCT-1998 (first entry)

XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 1..954

XX CDS /tag= a
 /product= "human RANKL (ligand for RANK)"

XX MO9828426-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23775.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI: 1998-377657/32.

XX P-PSDB: AAW69957.

XX New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells

XX Claim 25; Pages 59-60; 80pp; English.

XX This cDNA encodes a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumor necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists

sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other,

Query Match	47.38%	Score	96.4	DB	19	Length	954
Best Local Similarity	74.58%	Pred. No.	2.3e+23				
Matches	137	Conservative	0	Mismatches	41	Indels	5

QY	3	TEAGGCTGCTATAAAGAGTCCTTCTCTTGGAAACATGACCAAGATGGGCAAAAGTC	62
Db	531	TTGTTTCCCAATAAGTAGAGTCCTCTCTTGGTACCATATCGGGTTGGGCCAAGATTC	590
QY	63	CAACATGACTTCAGCAACGGAAACTAAGAGTCA-----AAGCACTTTTATACCGAA	116
Db	591	CAACATGACTTTACCAATGAAATATAGTAATACAGATGGCTTTATTAACTCGTA	650
QY	117	TGCGGACATTTTGCTTCGACATCGGATACCTCGACAGAGCCTAACCTGCGAGAGCTTCA	176
Db	651	TGCCAACATTTTGCTTTGACATCATGAAACTTCAGAGAGCCTACCTACAGAGATCTTCA	710
QY	177	GCTA 180	
Db	711	ACTA 714	

RESULT 5	
AAV41372	
ID	AAV41372 standard; cDNA; 954 BP.
XX	

08-OCT-1998 (first entry)

[illegible]

KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
XX

Homo sapiens.

key	Location/Qualifiers
FT	1..954
FT	44..

```
/product= "human RANKL (ligand for RANK)"
```

W09828424-A2.

PD 02-JUL-1998
YY

22-DEC-1997; 97WO-US23866

14-OCT-1997; 97US-0064671.

07-MAR-1997; 97US-0813509.

(IMMV) IMMUNEX CORP

Anderson DM, Galibert LJ, Maraskovsky E,

WP1; 1998-377655/32.
P-PSDB: AAW68293

New isolated recenter activator of

PT for, e.g. developing products for regulating an immune or
PM inflammatory response, treating toxic shock or sepsis
XX
PS
XS

Example 7: Pages 59-60; 80pp; English.

This cDNA encodes a human RANKL, a ligand for the RANK (receptor activator of necrosis factor- κ B) (NF- κ B) family peptide. RANK is a member of the tumor necrosis factor (TNF) family. Host cells transfected or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF- κ B, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF- κ B by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.

Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match	47.3%;	Score 96.4;	DB 19;	Length 954;
Best Local Similarity	74.5%;	Pred. No. 2.3e-23;		
Matches 137;	Conservative	0;	Mismatches 41;	Indels 6;
				Gaps 1

QY 3 TAGAGCTATAAAGATGCTTTCCTTGCAACATGCACAAGATTGGCAAAGCTC 62
|| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 531 TGGTTCCCATTAAGATGACTGTCTCTCTTGGTACCACATGATGGGGTTGGGCCAAAGATCTC 590

Ov	117	TCCGCGCACTTTCGGCAGGATTTATTACCGTA	650
Dd	591	CACATGCATTTTTAGCATGGAACATATGTAAICAGAGTGCTTTATTACCGTA	
Xj	63	CACATGCATTTTCAGCACGCGAAAACHTAAGTGTA-----AMGCCATTTATTAACCGAA	116

Accession	Sequence	Position
52	127 TGGCAGCATTTGCTTCGACATCGGGTAACTCTGACAGAGCCCTAACTCTGACAGACCTTCA	176
Db	651 TGGCAGCATTTGCTTCGACATCGGTAACCTTCAGAGAGACCTAGCTACAGAGTATCTTCA	710
GV	177 GCTA	180

Db	711	ACTA	714
----	-----	------	-----

```

RESULT 6
AADI5311
ID      AADI5311 standard; cDNA; 954 BP
XX

```

15-NOV-2001 (first entry)

XX
XX
..... receptor activator of NF- κ B ligand (RANKL) cDNA

KM tumour necrosis factor- α ; nuclear factor kappaB ligand; RANKL; NF;
KM immune response; TNF; TNF receptor associated factor; TRAF;
KM toxic shock; sepsis; acute inflammatory response; graft-versus-host reaction;
KM anti-apoptotic signal; therapy; immunosuppressant; bone resorption;
X anti-inflammatory; ss

Homo sapiens.

EH	Key	Location/Qualifiers
ET	CDS	1 OF 4

13

PN US6271349-B1.

07-AUG-2001.

17-DEC-1998; 98US-0215649.

Db 651 TGCCACACATTTGCTTGCATCATGAAACTTCAGGACCTAGCTACAGATATCTTCA 710
 QY 177 GCTA 180
 |||
 Db 711 ACTA 714

RESULT 8

AAD05904
 ID AAD05904 standard; cDNA: 954 BP.

AC AAD05904;

DT 31-JUL-2001 (first entry)

DE Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.

XX Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopontin;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; BP; cytostatic; chromosome 13q14;
 KW ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..954

FT /tag= a
 FT /product= "Human full-length RANKL (receptor activator
 of NF-kappaB ligand) protein"

W0200136637-A1.

25-MAY-2001.

14-NOV-2000; 2000WO-US31459.

17-NOV-1999; 99US-0442029.

(IMMUNEX CORP.

Anderson DM, Hughes AE;

WPI; 2001-329222/34.

P-PSDB; AAEO1993.

New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 Example 7; Page 75-76; 96pp; English.

The present invention relates to a novel receptor, referred to as RANK
 (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
 (tumour necrosis factor) receptor superfamily. RANK is a Type I
 transmembrane protein that interacts with TNF receptor-associated
 factors (TRAFs). Triggerting of RANK by overexpression or co-expression
 of RANK and membrane bound NF-kappaB (RANKL) results in upregulation
 of the transcription factor NF-kappaB, a ubiquitous transcription factor
 that is most extensively utilised in cells of the immune system.
 Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
 negative effects of inflammatory reactions, and the effects of excess
 bone resorption. The RANK DNAs, proteins and their analogues are useful
 for the preparation of pharmaceutical compositions, for infecting target
 cells for use in gene therapy applications in diagnosing diseases
 associated with RANK, and as targets for use in screening assays. They
 may be used in the treatment or diagnosis of immune system dysfunction.
 The present invention also encompasses gene therapy methods to correct
 gene-activating mutations, associated with e.g. Familial expansile
 osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 present sequence is a cDNA encoding full-length human RANKL (huRANKL)

CC protein. The RANKL gene is located in chromosome 13q14.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 47.3%; Score 96.4; DB 22; Length 954;
 Best Local Similarity 74.5%; Pred. No. 2.3e-23;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATATAAAGAGCTTTCTTCTTGGAAACATGACCAAGATTTGGCAACGCTTC 62

Db 531 TGGTCCCATTAAGAGATGCTCTCTTGGTACCATGATCGGCTTGGCCAAAGATCTC 590

QY 63 CAACATGACTTTGACGAACGAAACCTAAGAGTCA-----AAGCATTTATTACCGGAA 116

Db 591 CAACATGACTTTTGTAGCAATGAAACCTAATAGTTAATCAGATGCTTTTATTACCTGTA 650

QY 117 TGCCGACATTTGCTCTGACATCGGTAACCTCAGCAGGCTTAACCTGACGAGACTTCA 176

Db 651 TGCCACACATTTGCTTGCATCATGAAACTTCAGGACCTAGCTACAGATATCTTCA 710

QY 177 GCTA 180

|||

Db 711 ACTA 714

RESULT 9

ABK12877

ID ABK12877 standard; cDNA: 1945 BP.

AC ABK12877;

DT 18-JUN-2002 (first entry)

DE cDNA encoding human TRANCE protein splice variant 2.

XX Human; tumour necrosis factor-related activation induced cytokine;
 KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
 KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
 KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
 KW exostosis bursitis; multiple osteochondritis; exostosis; chondrocyte;
 KW cartilage growth; skeletal growth; gene; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT misc_feature 81..131

FT /tag= a
 FT /note= "Tumour necrosis factor (ligand) superfamily,
 member 11 (TNFSF11), Specifically claimed in
 claim 4"

FT misc_feature 81..140

FT /tag= b
 FT /note= "Target region for antisense nucleic acid"

FT CDS 95..829

FT /tag= c
 FT /product= "Human TRANCE (tumour necrosis factor-related
 activation induced cytokine) protein,
 splice variant 2"

W0200216551-A2.

28-FEB-2002.

20-AUG-2001; 2001WO-US26101.

18-AUG-2000; 2000US-226197P.

(UTMA-) UNIV MASSACHUSETTS MEDICAL CENT.

Choi Y, Odgren PR, Marks SC;

WPI; 2002-304119/34.

P-PSDB; AAU78286.

XX	Treating mammal having disorder characterised by abnormal
PT	cattle/skeletal growth such as dwarfism, acromegaly, by
PT	administering tumour necrosis factor-related activation induced
PT	cytokine-modulating agent to mammal -
XX	
PS	Disclosure: Fig 3; 55pp; English.
XX	
CC	The present invention relates to a new method of treating a mammal
CC	having a disorder comprising insufficient or excessive cartilage or
CC	skeletal growth. The method of the invention involves administering to
CC	the mammal a tumour necrosis factor-related activation induced cytokine
CC	(TRANCE)-modulating agent. The method is useful for treating a mammal
CC	having a disorder comprising insufficient or excessive cartilage or
CC	skeletal growth, where the disorder comprising insufficient cartilage
CC	or skeletal growth is selected from dwarfism, osteopetrosis,
CC	craniofacial-skeletal discrepancies and bone or cartilage damage
CC	resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
CC	arthritis, and disorders comprising excessive cartilage or skeletal
CC	growth are selected from acromegaly, gigantism, exostosis, cartilaginea,
CC	exostosis bursaia and multiple osteocartilaginous exostoses. The method
CC	is useful for inhibiting chondrocyte differentiation. The present
CC	nucleic acid sequence encodes the human TRANCE protein, splice variant
CC	2, of the invention. TRANCE is a member of the tumour necrosis factor
CC	family and acts directly on cartilage-producing cells (chondrocytes).
SQ	Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other:
OY	Query Match 47.3%; Score 96.4; DB 24; Length 1945;
Db	Best Local Similarity 74.5%; Pred. No. 3e-23;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;	
OY	3 TGAGCGTCATPAAACGAGCTTCTTCTTGGAACAATGACCAGATTGGGCANACGTCTC 62
Db	406 TGGTTCCCATTAATGAGTGTCTCTTGCTATGACATGATCGGGGTTGGCCAAGATCTC 465
OY	63 CAACATGACTTTCAGCAACGGAANAATAAGATCA-----AAGCATTTATTAACGGGAA 116
Db	466 CAACATGACTTTTGACATGGAAGAACAATAGTTAATCAGATGGCTTTATTAATTCGTA 525
OY	117 TGGCGACATTTGCTCTGCACATGCCGATTAACCTCAGACGGCTTAATCTGCAGACCTTCA 176
Db	526 TGGCAACATTTGGCTTTCGACATCATGAACATTCAGAGAGACTTACTACAGATGATCTTCA 585
OY	177 GCTA 180
Db	586 ACTA 589
RESULT 10	
ABK12876	
ID	ABK12876 standard; CDNA: 2226 BP.
AC	
XX	ABK12876;
DT	
XX	18-JUN-2002 (first entry)
DE	
XX	CDNA encoding human TRANCE protein splice variant 1.
XX	
KW	Human: tumour necrosis factor-related activation induced cytokine;
KW	TRANRC: dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
KW	bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
KW	rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilaginea;
KW	exostosis bursaia; multiple osteocartilaginous exostosis; chondrocyte;
KW	cartilage growth; skeletal growth; gene; ss.
OS	Homo sapiens.
XX	
FH	Key
FT	misc_feature
FT	location/Qualifiers
FT	141..190
FT	/tag= a
FT	"tumour necrosis factor (ligand) superfamily
FT	member 11 (TNFSF11), target region for antitumour

FT	CDS		157..1110	nucleic acid. Specifically claimed in claim 4"
FT			/+tag- b	
FT			/product=	"Human TRANCE (tumour necrosis factor-related
FT				activation induced cytokine) protein,
FT				splice variant 1"
XX				
PN			WO200216551-A2.	
XX				
PD			28-FEB-2002.	
XX				
PF			20-AUG-2001; 2001WO-US26101.	
XX				
PR			18-AUG-2000; 2000US-226197P.	
XX				
PA			(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.	
PI				
XI			Choi Y, Odgren PR, Marks SC:	
XX				
DR			WPI; 2002-304119/34.	
P			P-PsDB; AA078285.	
PT			Treating mammal having disorder characterised by abnormal	
PT			cartilage/skeletal growth such as dwarfism, acromegaly, by	
PT			administering tumour necrosis factor-related activation induced	
PT			cytokine-modulating agent to mammal -	
PS			Disclosure; Fig 1; 55pp; English.	
XX				
CC			The present invention relates to a new method of treating a mammal	
CC			having a disorder comprising insufficient or excessive cartilage or	
CC			skeletal growth. The method of the invention involves administering to	
CC			the mammal a tumour necrosis factor-related activation induced cytokine	
CC			(TRANCE)-modulating agent. The method is useful for treating a mammal	
CC			having a disorder comprising insufficient or excessive cartilage or	
CC			skeletal growth, where the disorder comprising insufficient cartilage	
CC			or skeletal growth is selected from dwarfism, osteopetrosis,	
CC			craniofacial-skeletal discrepancies and bone or cartilage damage	
CC			resulting from traumatic injury, surgery, osteoarthritis or rheumatoid	
CC			arthritis, and disorders comprising excessive cartilage or skeletal	
CC			growth are selected from acromegaly, gigantism, exostosis, cartilageinae,	
CC			exostosis bursata and multiple chondrocyte differentiation. The method	
CC			is useful for inhibiting chondrocyte differentiation. The present	
CC			nucleic acid sequence encodes the human TRANCE protein, splice variant	
CC			1, of the invention. TRANCE is a member of the tumor necrosis factor	
CC			family and acts directly on cartilage-producing cells (chondrocytes).	
SQ			Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;	
XX				
XX				
Query Match		47.3%; Score 96.4; DB 24; Length 2226;		
Best local Similarity		74.5%; Pred. No. 3.2e-23;		
Matches 137; Conservative		0; Mismatches 41; Indels 6; Gaps		
OY				1.
	3	TGAGGCTCAATAACGAGCTTCTTTCTTGGAACATGACCAGATGGCGCAACGCTTC	62	
Db	687	TGGTTCCTCAAAAGTAGTCTCTCTCTGTGACCATGATCGGGGTGGCCAAGATCTC	746	
OY				
	63	CACCATGACTTTCAGCAGCAAGAAAACCTAAGACTCA-----AAGGCATTATTACCGGAA	116	
Db	747	CACATGACTTTTACGAAATGAGAAACTAATATTATATCAGGATGGCTTTATTACCTGTA	806	
OY				
	117	TGCCGACATTTGCTGTCGACATCGGCTCACACAGGCGCTAACCTCGACGACCTTCA	176	
Db	807	TGCGAACATTTGCTTGACATCATGAAACTTCAGAGACCTAGCTACAGAGTATCTTCA	866	
OY				
	177	GCTA 180		
Db	867	ACTA 870		
RESULT 11				
AAZ99964				
ID	AAZ99964	standard; DNA; 2271 BP.		

```

XX AC AA299964;
XX XX 25-JUL-2000 (first entry)
XX XX
DE DNA encoding a human osteoprotegerin ligand (OPGL).
XX XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 185..1138
FT /tag= a
FT /product= "osteoprotegerin ligand"
XX PN MO200015807-A1.
XX XX
XX PD 23-MAR-2000.
XX XX
XX PF 13-SEP-1999; 99WO-DK00481.
XX XX
XX PR 15-SEP-1998; 98DK-0001164.
XX PR 02-OCT-1998; 98US-0102896.
XX XX
XX PA (MEBI-) M & E BIOTECH AS.
XX XX
XX PI Halkier T, Haaning J;
XX XX
XX DR WPI: 2000-271444/23.
XX DR P-PSDB; AAY84417.
XX XX
XX PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX XX to treat, prevent and ameliorate osteoporosis -
XX PS Disclosure; Page 75-77; 110pp; English.
XX XX
XX CC The present sequence encodes a human osteoprotegerin ligand (OPGL).
XX CC Osteoprotegerin is a secreted member of the tumour necrosis factor
XX CC receptor family which blocks osteoclastogenesis in a dose dependent
XX CC manner. The OPGL protein is synthesised as a type II transmembrane
XX CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX CC is a potent osteoclast differentiation factor when combined with CSF-1.
XX CC It is not capable of inducing osteoclast differentiation in the absence
XX CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX CC specification describes a method for the in vivo down-regulation of
XX CC OPGL activity in an animal. The method comprises using at least one OPGL
XX CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
XX CC an immune response in the animal. The method and OPGL polypeptide are
XX CC useful for treating, preventing and ameliorating osteoporosis or other
XX CC diseases or conditions characterised by excessive bone resorption.
XX XX
XX SQ Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;

```

```

Query Match 47.3%; Score 96.4; DB 21; Length 2271;
Best Local Similarity 74.5%; Pred. No. 3.2e-23;
Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

```

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OY 3 TGAGGCTCATAAAGAGAGCTTCTTCTTGGAACATGACCAAGATTGGCAACGCTCTC 62
DB 715 TGGTTCCTCCATAAGAGAGCTCTCTCTTGGAACATGATCGGGTGGCAAGATCTC 774
OY 63 CAACATGACTTTCACCAAGCAAGAACTAAGAGTCA-----AAGGATTTATTACCGGAA 116
DB 775 CAACATGACTTTCACCAAGCAAGAACTAAGTATATATACGATGGCTTTATTACCTGTA 834
OY 117 TGGCGACATTTGCTGCACATCGGTAACCTCAGACAGCCTTAAGTCTGACGACCTTCA 176
DB 835 TGGCGACATTTGCTGCACATCATGAAATCTGAGAGACCTAGCTAAGAGTATCTTCA 894

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OY 177 GCTA 180
DB 895 ACTA 898

```

RESULT 12
AAV70285
ID AAV70285 standard; DNA; 2274 BP.
AC AAV70285;
XX 11-FEB-1999 (first entry)
XX XX
DE Human osteoprotegerin binding protein from the pcDNA/huOPSP1.insert.
XX XX
KW Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease; ss.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 185..1138
FT /tag= a
FT /product= "osteoprotegerin binding protein"
XX PN MO9846751-A1.
XX XX
XX PD 22-OCT-1998.
XX XX
XX PF 15-APR-1998; 98WO-US07584.
XX XX
XX PR 30-MAR-1998; 98US-0052521.
XX PR 16-APR-1997; 97US-0842842.
XX PR 23-JUN-1997; 97US-0880855.
XX XX
XX PA (AME-) AMGEN INC.
XX XX
XX PI Boyle WJ;
XX XX
XX DR WPI: 1998-594578/50.
XX DR P-PSDB; AAM83195.
XX XX
XX PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
XX XX e.g. treating bone diseases by modulating osteoclast differentiation
XX XX and for diagnosis
XX PS Claim 1; Fig 4; 47pp; English.
XX XX
XX CC The present sequence encodes human osteoprotegerin (OPB) binding protein.
XX CC Host cells transfected with vectors containing nucleic acid molecules
XX CC encoding OPB binding protein are used to produce recombinant OPB binding
XX CC protein. OPB binding protein is used in binding assays to determine
XX CC osteoprotegerin (OPB) in biological samples; to screen for specific
XX CC binding agents (particularly agonists and antagonists, including
XX CC intracellular proteins); to raise Ab (useful in immunoassays for
XX CC detection of OPB binding protein) and to identify compounds that
XX CC modulate binding of OPB binding protein to osteoclast differentiation
XX CC and activation receptor (ODAR). The nucleic acid molecule encoding OPB
XX CC binding protein can be used to detect OPB binding protein-encoding
XX CC sequences, e.g. screening for related sequences, also to produce
XX CC transgenic animal models, while complementary sequences are used for
XX CC antisense regulation of OPB binding protein expression. Modulators of
XX CC OPB binding protein, particularly soluble forms of OPB binding protein
XX CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
XX CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
XX CC disease, periodontal disease, osteoporosis, loosening of prostheses,
XX CC optionally in combination with agents that promote bone growth.
XX SQ Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

```

Query Match 47.3%; Score 96.4; DB 19; Length 2274;

```


Tue Dec 10 10:51:35 2002

us-09-880-457-1_copy_543_746.rge

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 16:41:40 : Search time 436.856 Seconds
(without alignments)
13590.225 Million cell updates/sec

Title: us-09-880-457-1_COPY_543_746
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : GenBank:
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2: gb_hcg:*
3: gb_lo:*
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40: gb_lo:*
41: gb_lo:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	194	95.1	1186	6	AX358828
2	194	95.1	1186	6	AX362321
3	194	95.1	165707	2	AC104794
4	194	95.1	190748	9	AC010969
5	96.4	47.3	818	9	AB064268
6	96.4	47.3	911	9	AB061227
7	96.4	47.3	930	9	AB037599
8	96.4	47.3	954	6	AR156414
9	96.4	47.3	954	6	AR164148
10	96.4	47.3	954	6	AX451895
11	96.4	47.3	972	9	AB064270
12	96.4	47.3	1034	9	AB064269
13	96.4	47.3	1034	9	AF053712
14	96.4	47.3	1034	9	AF053712
15	96.4	47.3	1034	9	AF053712
16	96.4	47.3	1034	9	AF053712
17	96.2	47.2	113451	2	AC023297
18	96.2	47.2	200724	9	AF139382
19	93.2	45.7	1823	9	AF131711
20	84	41.2	957	10	AF187319
21	84	41.2	127812	2	AC094149
22	80.8	39.6	754	10	AB032772
23	80.8	39.6	864	10	AB032771
24	80.8	39.6	951	6	E34350
25	80.8	39.6	951	6	E36388
26	80.8	39.6	951	10	AB036798
27	80.8	39.6	951	10	AB036798
28	80.8	39.6	1630	6	AR156433
29	80.8	39.6	1630	6	AR164147
30	80.8	39.6	1630	6	AX147987
31	80.8	39.6	1694	6	AX451897
32	80.8	39.6	2029	6	E34349
33	80.8	39.6	2029	10	AB022039
34	80.8	39.6	2191	6	AR157058
35	80.8	39.6	2191	6	AX140162
36	80.8	39.6	2225	10	AF019048
37	80.8	39.6	2225	10	AF019048
38	80.8	39.6	2225	10	AF019048
39	80.8	39.6	2225	10	AF019048
40	80.8	39.6	2225	10	AF019048
41	80.8	39.6	2225	10	AF019048
42	80.8	39.6	2225	10	AF019048
43	80.8	39.6	2225	10	AF019048
44	80.8	39.6	2225	10	AF019048
45	80.8	39.6	2225	10	AF019048

ALIGNMENTS

RESULT 1
AX358828
LOCUS
DEFINITION
AX358828
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gilmaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K., and Wood, W.I.

Pred. No. is the number of results predicted by chance to have a

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0193983-A 81 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES Location/Qualifiers
 source 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 95.1%; Score 194; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 3.8e-53;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGAGGCTCATAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 DB 504 CATGAGGCTCATAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 OY 61 TCCACATGACTTTCAGCAACGAAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 DB 564 TCCACATGACTTTCAGCAACGAAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 OY 121 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTCTGACAGCTTCAGCTA 180
 DB 624 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTCTGACAGCTTCAGCTA 180
 OY 181 TGGTGTATTGAG 194
 DB 684 TGGTGTATTGAG 697

RESULT 2 AX362321 1186 bp DNA linear PAT 15-FEB-2002
 LOCUS AX362321
 DEFINITION Sequence 81 from Patent WO0208288.
 ACCESSION AX362321
 VERSION AX362321.1 GI:18694618
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 81 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
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Query Match 95.1%; Score 194; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 3.8e-53;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGAGGCTCATAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 DB 504 CATGAGGCTCATAAACGAGTCTTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
 OY 61 TCCACATGACTTTCAGCAACGAAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 DB 564 TCCACATGACTTTCAGCAACGAAACCTAAGAGTCAAGAGCATTTATTACCGAATGCC 120
 OY 121 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTCTGACAGCTTCAGCTA 180
 DB 624 GACATTGGCTCTCGACATCGCGTAACTCAGACGCGCTAAGCTCTGACAGCTTCAGCTA 180

OY 181 TGGTGTATTGAG 194
 DB 684 TGGTGTATTGAG 697

RESULT 3 AC104794 165707 bp DNA linear HTG 30-APR-2002
 LOCUS AC104794
 DEFINITION Homo sapiens chromosome 2 clone RP11-254F7, WORKING DRAFT SEQUENCE.
 AC104794
 AC104794.3 GI:20340520
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 3 (bases 1 to 165707)
 Waterston, R.H.
 Direct Submission
 Submitted (30-APR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Apr 30, 2002 this sequence version replaced gi:19339129.

REFERENCE 1 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Apr 30, 2002 this sequence version replaced gi:19339129.

COMMENT

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 Project Information
 Center project name: H_NH0254F07

Summary Statistics
 Sequencing vector: M13; 0%
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 162662 bases at least Q40
 Consensus quality: 163189 bases at least Q30
 Insert size: 9479; agarose-fp
 Insert size: 167795; sum-of-contigs
 Quality coverage: 12.78 in Q20 bases; agarose-fp
 Quality coverage: 10.53 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 3 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1112: contig of 1112 bp in length
 * 1113 1212: gap of unknown length
 * 1213 76227: contig of 75015 bp in length
 * 76228 76327: gap of unknown length
 * 76328 165707: contig of 89380 bp in length.
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 source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4,2e-53;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATGAGCTCATTAACGACGCTTCTTCTTGGAACATGACCAAGATTGGCAACGCTC 60
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DB 41177 CATGAGCTCATTAACGACGCTTCTTCTTGGAACATGACCAAGATTGGCAACGCTC 41236
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QY 61 TCCACATGACTTTCAGCAACGAAACTAGAGTCAAGGCTTTTACCGGATGCC 120
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DB 41237 TCCACATGACTTTCAGCAACGAAACTAGAGTCAAGGCTTTTACCGGATGCC 41236
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QY 121 GACATTTGCTCTGCACATGCGCTAACCTAGAGGCTTAACCTGAGACCTTCAGCTA 180
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DB 41297 GACATTTGCTCTGCACATGCGCTAACCTAGAGGCTTAACCTGAGACCTTCAGCTA 41356
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QY 181 TGGTGAATTGAG 194
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DB 41357 TGGTGAATTGAG 41370
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RESULT 4
AC010969/c      AC010969      190748 bp      DNA      linear      PRI 07-NOV-2001
LOCUS      Homo sapiens BAC clone RP11-95D17 from 2, complete sequence.
DEFINITION      AC010969
ACCESSION      AC010969.11 GI:13677120
VERSION      HTG.
KEYWORDS      Homo sapiens.
SOURCE      Homo sapiens.
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Sultston,J.E. and Waterston,R.
              Toward a complete human genome sequence
              Genome Res. 8 (11), 1097-1108 (1998)
              99063792
MEDLINE      PUBMED
              9847074
              2 (bases 1 to 190748)
REFERENCE      Sun,H., Abbott,A. and Je,T.P.
              The sequence of Homo sapiens BAC clone RP11-95D17
              JOURNAL      Unpublished
              3 (bases 1 to 190748)
REFERENCE      Waterston,R.H.
              Direct Submission
              Submitted (28-SEP-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              4 (bases 1 to 190748)
REFERENCE      Waterston,R.H.
              Direct Submission
              Submitted (19-APR-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
              5 (bases 1 to 190748)
REFERENCE      Waterston,R.H.
              Direct Submission
              Submitted (20-APR-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA

```

REFERENCE

6 (bases 1 to 190748)
 Waterston,R.
 Direct Submission
 Submitted (07-NOV-2001) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Apr 19, 2001 this sequence version replaced gi:11128441.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Center file: http://genome.wustl.edu/gsc
 Web site: http://genome.wustl.edu
 Contact: sapiens@wustl.edu
 ----- Summary Statistics
 Center project name: H.NH0095D17

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., paired quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
 donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
 Tateno,M., Catanesi,J.J. and de Jong,P.J. (1996) An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
 and coworkers at the Roswell Park Cancer Institute
 (http://bacpac.med.buffalo.edu)

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-521D12. Actual start of
 this clone is at base position 1 of RP11-95D17; actual end is at
 base position 190748 of RP11-95D17.

There are polymorphic base differences between RP11-95D17 and the
 redundant clone AC062035. Data from AC062035 was used to finish
 RP11-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Size
 information from restriction digest suggests that the full repeat
 may not be represented.

FEATURES

source

Location/Qualifiers
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 /clone_id="RP11-11"

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repeat_region
 325..805
 /rpt_family="L1"

repeat_region
 806..1114
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repeat_region
 1449..1567
 /rpt_family="MIR"

repeat_region
 2179..2369

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misc_feature      14205..14259
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repeat_region      14851..15156

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Query Match      95.18; Score 194; DB 9; Length 190748;
Best Local Similarity 100.0%; Pred. No. 4.2e-53;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CATGAGGCTCATAAACGAGCTTTCTTGGAAACATGACCAAGATTGGGCAACGTC 60
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Db 174428 CATGAGGCTCATAAACGAGCTTTCTTGGAAACATGACCAAGATTGGGCAACGTC 174369
QY 61 TCCAACTGACTTTCAGCAACGAAACTAAGAGTCAAGGCAATTTATTCGGGAATGCC 120
|||||
Db 174368 TCCAACTGACTTTCAGCAACGAAACTAAGAGTCAAGGCAATTTATTCGGGAATGCC 174309
QY 121 GACATTTGCTCTGCAACGCTGTAACCTGACGAGGCTTAACCTGAGGACCTTCAGCTA 180
|||||
Db 174308 GACATTTGCTCTGCAACGCTGTAACCTGACGAGGCTTAACCTGAGGACCTTCAGCTA 174249
QY 181 TGGGTGAATTTGAG 194
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Db 174248 TGGGTGAATTTGAG 174235

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RESULT 5      818 bp mRNA linear PRI 26-DEC-2001
AB064268      kappa B ligand 3, complete cds.
LOCUS          AB064268
DEFINITION    Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor
ACCESSION     AB064268
VERSION       AB064268.1 GI:18143616
KEYWORDS      Homo sapiens cDNA to mRNA.
SOURCE        Homo sapiens
ORGANISM      Homo sapiens

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REFERENCE     Ikeda,T., Kuroyama,H. and Hirokawa,K.
AUTHORS      Determination of human RANKL isoforms
TITLE        2 (bases 1 to 818)
AUTHORS      Ikeda,T. and Kuroyama,H.
TITLE        Direct Submission
JOURNAL       Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
              University, Department of Pathology and Immunology, Graduate
              School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
              (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176,
              Fax:81-3-5803-0123)

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source
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Location/Qualifiers

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 Query Match 47.3%; Score 96.4; DB 9; Length 818;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

OY 3 TGAGGCTCATTAAGAGAGCTTTCTTCTTGGAAACATGACCAATGGGCAACGCTC 62
 DB 395 TGGTTCATTAAGAGAGCTTTCTTCTTGGTACATGATGGGGTGGCCAAAGATCTC 454
 OY 63 CAACATGACTTTCAGCAACGGAAGAACTAAGATCA-----AAGGCATTATTAACCGGAA 116
 DB 453 CAACATGACTTTCAGCAACGGAAGAACTAAGATCAAGATGAGTGGCTTTTATTAACCTGTA 514
 OY 117 TGCCGACATTTGCTCTCGACATCGGTAACTGACAGGCTTAAGCTTTCGACGGACCTTCA 176
 DB 515 TGCCGACATTTGCTCTCGACATCGGTAACTGACAGGCTTAAGCTTTCGACGGACCTTCA 574
 OY 177 GCTA 180
 DB 575 ACTA 578

RESULT 6
 LOCUS AB061227 911 bp mRNA linear PRI 03-NOV-2001
 DEFINITION Homo sapiens mRNA for hRANKL 2, complete cds.
 AB061227
 AB061227.1 GI:16610212

KEYWORDS
 SOURCE Homo sapiens cDNA to mRNA.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 Ikeda, T., Kuroyama, H. and Hirokawa, K.
 TITLE Human RANKL Isoform
 JOURNAL Unpublished
 2 (bases 1 to 911)
 AUTHORS Ikeda, T. and Kuroyama, H.
 TITLE Direct Submission
 JOURNAL Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical
 and Dental University Pathology and Immunology; 1-5-45 Yushima,
 Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: coru.phn2@med.tmd.ac.jp,
 Tel:81-3-5803-5176, Fax:81-3-5803-0123)

FEATURES
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 GFYLVANICFRHHTSGDLAT EYLQLMVYVTKTSIKIPSSHTLMKGSSTYWSGNSSEHF
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 Query Match 47.3%; Score 96.4; DB 9; Length 911;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

OY 3 TGAGGCTCATTAAGAGAGCTTTCTTCTTGGAAACATGACCAATGGGCAACGCTC 62
 DB 488 TGGTTCATTAAGAGAGCTTTCTTCTTGGTACATGATGGGGTGGCCAAAGATCTC 547
 OY 63 CAACATGACTTTCAGCAACGGAAGAACTAAGATCA-----AAGGCATTATTAACCGGAA 116
 DB 548 CAACATGACTTTCAGCAACGGAAGAACTAAGATCAAGATGAGTGGCTTTTATTAACCTGTA 607
 OY 117 TGCCGACATTTGCTCTCGACATCGGTAACTGACAGGCTTAAGCTTTCGACGGACCTTCA 176
 DB 608 TGCCGACATTTGCTCTCGACATCGGTAACTGACAGGCTTAAGCTTTCGACGGACCTTCA 667
 OY 177 GCTA 180
 DB 668 ACTA 671

RESULT 7
 LOCUS AB037599 930 bp mRNA linear PRI 19-MAR-2002
 DEFINITION Homo sapiens mRNA for SODF/TRANCE, complete cds.
 AB037599
 AB037599.1 GI:6863047

KEYWORDS
 SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma
 cell_line:SCC-4 cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 Nagai, M., Kyakumoto, S. and Sato, N.
 TITLE Cancer cells responsible for humoral hypercalcemia express mRNA
 encoding a secreted form of ODF/TRANCE that induces osteoclast
 formation
 JOURNAL Biochem. Res. Commun. 269 (2), 532-536 (2000)
 20175237
 2 (bases 1 to 930)
 AUTHORS Nagai, M., Kyakumoto, S. and Sato, N.
 TITLE Direct Submission
 JOURNAL Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University
 School of Dentistry, Department of Biochemistry; 19-1 Uchinaru,
 Morioka, Iwate 020-8505, Japan (E-mail:mnagai@iwate-med.ac.jp,
 Tel:+81-19-651-5111(ex. 4436), Fax:+81-19-654-4147)

FEATURES
 source location/Qualifiers

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 PGSKHVSLSSWYHDSGMKAKISNMTFSNKLIVNDGFYLVANICFRHHTSGDLAT
 EYLQLMVYVTKTSIKIPSSHTLMKGSSTYWSGNSSEHFYSINVGFFKLRSGEISI
 EVSNPSLDLPDDATYFGAFKVRDID"
 EVSNPSLDLPDDATYFGAFKVRDID"

BASE COUNT 283 a 184 c 200 g 260 t
 ORIGIN
 Query Match 47.3%; Score 96.4; DB 9; Length 930;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 406 TGGTCCCATTAAGAGAGCTGCTCTTGTGTAACATGATCGGGTTGGGCCAAGATCTC 465
 QY 63 CAACATGACTTTGACCAAGCAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 466 CAACATGACTTTTACCAATGGAATACTAATAGTATATCAGATGGCTTTATTACCTGTA 525
 QY 117 TGGCGACATTTGCTCTGACATCGGTAACCTCAGACGCTTAACCTGACGAGCTTCA 176
 Db 526 TGGCAACATTTGCTTTCACATCATGAAACTTCAGAGACCTAGCTACAGATATCTTCA 585
 QY 177 GCTA 180
 Db 586 ACTA 589

RESULT 8
 ARI56434
 LOCUS ARI56434 954 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 12 from patent US 6242213.
 ACCESSION ARI56434
 VERSION ARI56434.1 GI:15125138
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 954)
 AUTHORS Anderson,D.M.
 TITLE Isolated DNA molecules encoding RANK-L
 JOURNAL Patent: US 6242213-A 12-05-JUN-2001;
 FEATURES Location/Qualifiers
 source 1..954

BASE COUNT 255 a 239 c 227 g 233 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 6; Length 954;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 531 TGGTCCCATTAAGAGAGCTGCTCTTGTGTAACATGATCGGGTTGGGCCAAGATCTC 590
 QY 63 CAACATGACTTTGACCAAGCAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 591 CAACATGACTTTTACCAATGGAATACTAATAGTATATCAGATGGCTTTATTACCTGTA 650
 QY 117 TGGCGACATTTGCTCTGACATCGGTAACCTCAGACGCTTAACCTGACGAGCTTCA 176
 Db 651 TGGCAACATTTGCTTTCACATCATGAAACTTCAGAGACCTAGCTACAGATATCTTCA 710
 QY 177 GCTA 180
 Db 711 ACTA 714

RESULT 9
 ARI64148
 LOCUS ARI64148 954 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 12 from patent US 6271349.
 ACCESSION ARI64148
 VERSION ARI64148.1 GI:16235114
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 954)
 AUTHORS Douglall,W.C. and Galibert,L.
 TITLE Receptor activator of NF- κ B
 JOURNAL Patent: US 6271349-A 12-07-AUG-2001;
 FEATURES Location/Qualifiers

source 1..954
 BASE COUNT 255 a 239 c 227 g 233 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 6; Length 954;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 531 TGGTCCCATTAAGAGAGCTGCTCTTGTGTAACATGATCGGGTTGGGCCAAGATCTC 590
 QY 63 CAACATGACTTTGACCAAGCAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 591 CAACATGACTTTTACCAATGGAATACTAATAGTATATCAGATGGCTTTATTACCTGTA 650
 QY 117 TGGCGACATTTGCTCTGACATCGGTAACCTCAGACGCTTAACCTGACGAGCTTCA 176
 Db 651 TGGCAACATTTGCTTTCACATCATGAAACTTCAGAGACCTAGCTACAGATATCTTCA 710
 QY 177 GCTA 180
 Db 711 ACTA 714

RESULT 10
 AX147989
 LOCUS AX147989 954 bp DNA linear PAT 08-JUN-2001
 DEFINITION Sequence 12 from Patent WO0136637.
 ACCESSION AX147989
 VERSION AX147989.1 GI:14346964
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 954)
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL Receptor activator of nf- κ B
 Patent: WO 0136637-A 12-25-MAY-2001;
 FEATURES Immunex Corporation (US)
 source Location/Qualifiers
 1..954
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 1..954
 /note="unnamed protein product"
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 /db_xref="GI:14346965"
 /translation="MRRASRDYTKYLRSSEMGSGPAPHEPLAPPPAPPPAPPA
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 EAQPFALHTINATIDIPSGSHKYSLSMHRGRKAKISNPKSLIVMDGFRYYLYA
 NICEFRHETSGDLATEYLIOMYVVTSTIKTSRSLMKGSTKYSKNSSEHFYSIN
 VGFEFLRSGEELSTEVNSLDDPDQDAVTFGAFVRDID"

BASE COUNT 255 a 239 c 227 g 233 t
 ORIGIN

Query Match 47.3%; Score 96.4; DB 6; Length 954;
 Best Local Similarity 74.5%; Pred. No. 8.7e-21;
 Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 3 TGAGGCTCATAAAGAGCTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTTC 62
 Db 531 TGGTCCCATTAAGAGAGCTGCTCTTGTGTAACATGATCGGGTTGGGCCAAGATCTC 590
 QY 63 CAACATGACTTTGACCAAGCAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAA 116
 Db 591 CAACATGACTTTTACCAATGGAATACTAATAGTATATCAGATGGCTTTATTACCTGTA 650
 QY 117 TGGCGACATTTGCTCTGACATCGGTAACCTCAGACGCTTAACCTGACGAGCTTCA 176

Db
651 TGCCAACATTTGGCTTTCGACATCATGAACCTTCAGAGAGACCTGACTACAGAGATCTCTCA 710

Qy	177	GCTA	180
Db	711	ACTA	714

RESULT	11				
LOCUS	AX451895				
DEFINITION	Sequence 5 from Patent WO0224896.	954 bp	DNA	linear	PAT 03-JUL-2002
ACCESSION	AX451895				
VERSION	AX451895.1	GI:21698735			
KEYWORDS					

REFERENCE	1
AUTHORS	Dougall, W.C.
TITLE	Screening assays for agonists or antagonists of receptor activation of nf-kb
JOURNAL	Patent: WO 0224896-A 5 28-MAR-2002; IMMGENX CORPORATION (US)
FEATURES	location/Qualifiers
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	/db_xref="taxon:9606"
CDS	1..954
	1..954 "unnamed protein product"

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 /db_xref="GI:21698736"
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 TLESODTKLIPDSCRRIKQAFQGAQVKELOHIVSQHIRAKAMWDSMDLAKRSK
 EOPFAHLINATIDIPSGHSKYSLSWHDKRAMTISNTSNGCLLYNDQGFYVLA
 NICEFRHETSGDILATEYLOLMVYVTKTSIKIPSTLTKMGSTKIWSGNSSEPHYSIN
 VGSEFKLRSGEELSEIVSNPILDDPOATYTGAPKRVDDID"

[illegible]

RESULT 12			
AB064270	AB064270	972 bp mRNA	linear PRI 26-DEC-2001
Locus	Homo sapiens hRANKL 2-2	mRNA for receptor activator	of nuclear
DEFINITION	factor kappa B ligand 2-2,	complete cds.	
ACCESSION	AB064270		
VERSION	AB064270.1	GI:18143620	
KEYWORDS	Homo sapiens cDNA to mRNA.		
SOURCE			

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1	Ikeda, T., Kuroyama, H. and Hirokawa, K. Determination of human RANKL isoforms unpublished (bases 1 to 972)
REFERENCE 2	Ikeda, T. and Kuroyama, H. Direct Submission Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate

FEATURES	location/Qualifiers
source	1..972 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..972 /gene="hrankl 2-2"
CDS	160..972 /gene="hrankl 2-2"

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/codon_start=1
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/protein_id="BAB79695.1"
/db_xref="GI:18134621"
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EDGTCIYRLL
RIHERNADDPDPTLESODPKILIPDSCRIKQAFQGVQVKELOHIG
AISOHIREAKMVAVG
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SNMTFNSGKLL
VNQDGFYLYLVANICFRHHETSDSLATEYLOLMVYTKTSIKIPSH
TLMKSGKRWYS
GNSHFHYSYINGFFKLSRSGEISYENSLLDDPPDDAIFYGAFKVR
DID"

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	Query Match	47.3%	Score 96.4;	DB 9;	Length 912;
	Best Local Similarity	74.5%;	Pred. NO.	8.7e-21;	
Matches 137; Conservative		0;	Mismatches	41;	Indels Gaps 1;
OY	3 TGAAGCTCATAAAACGAGTCTTCCTCCTTTGGAAACATGCACMAAGATTGGCCCAACGTCTC	62			
Db	549 TGTTTTCCCATAAAGTAGTGACTGTGCCCTTGGTACCATGATCGGGGTTGGGCCCAAGATCTC	608			
OY	63 CAACATGACTTTTCGACAACGGAAGAATAAGAGTCA-----AAGSCATTATTACCGCAA	116			
Db	609 CAAATGACTTTTATGCAATGSAAMAACTAATAGTATTACAGAGTGGCTTTATTACCTCTA	668			
OY	117 TCGCGACATTTTGCTCTCGACATCGCGTAACCTCAGAGAGCGTAACTCTCACGAGACTTCA	176			
Db	669 TGCCAACATTTTGGCTTTGACATCATGAACCTTCAAGGAGACTTACGTACAGAGATTTCTCA	728			
OY	177 GGTA 180				
Db	729 ACTA 732				

[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1034).
Ikeda, T. and Kuroyama, H.
Direct Submission
Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Cell Biology, Graduate
School, Yushima 1-5-45, Bunkyo, Tokyo 113-8513, Japan
(E-mail: tohru.ph2@med.tmd.ac.jp, Tel: 81-3-5803-5176,
Fax: 81-3-5803-0123)

source	Location/Qualifiers
gene	1..1034 /organism="Homo sapiens" /db_xref="taxon:9606"
CDS	1..1034 /gene="hrankl 1" 81..1034

BASE COUNT	275 a	257 c	265 g	237 t
ORIGIN	"COLTANCSGELISLEYSNPSLDDPDQATYFGAFKVRDID"			

RESULT 14	AF019047	2201 bp	mRNA	linear	PRI 22-NOV-1997
LOCUS	AF019047	Homo sapiens	receptor activator of	nuclear factor	kappa B ligand
DEFINITION	AF019047				
ACCESSION	AF019047				
VERSION	AF019047.1	GI:2612921			
KEYWORDS					

REFERENCE 2 (bases 1 to 2271)

AUTHORS Boyle,W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES Location/Qualifiers

source

1..2271

/organism="Homo sapiens"

/db_xref="taxon:9606"

CDS

185..1138

/function="regulates osteoclast differentiation and activation"

/codon_start=1

/product="osteoprotegerin ligand"

/protein_id="AAC39731.1"

/db_xref="GI:3057146"

/translation="MRRASRDYTKYLRSSEMGSGPGAPHEGPLHAPPPAPHPAPPA
SRSEFVALGLGLGVCSVALFEYFRACMDPNRISDGTNCTYRILRLHENDFQDT
TLESODTKLIPDSGRITKQAFQGAQVQKLOHIVSOHIRAEKAMVDSWDLAKRSKL
EADPFALHTINADIPSGSHKYSLSMYHNRGMAKISNMTFSGKLIYNODGFYLYA
NICFRHETSGDIALEYLQLMVIVTKTSIKIPSSHILMKGSGTKYWSGNSSEFHYISIN
VGGFRLRSGEISIEVSNPSLDPDQDATYFAFVRRDID"

BASE COUNT 658 a 462 c 522 g 629 t

ORIGIN

Query Match 47.3%; Score 96.4; DB 9; Length 2271;

Best Local Similarity 74.5%; Pred. No. 8.8e-21; Mismatches 41; Indels 6; Gaps 1;

Matches 137; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

OY 3 TGAGGCTCATATAACAGAGCTCTTCTCTGGAACATGACCAAGATTGGGCAACGCTCTC 62

DB 715 TGTTCCTCCATAAGTAGTCTGCTCTCTGTGTACCATGATCGGGGTGGCCAAAGATCTC 774

OY 63 CAACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGGCATTATTACCGGAA 116

DB 775 CAACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGGCATTATTACCGGAA 834

OY 117 TGGCGACATTGGCTCTGCAATCGGCTAACCCTGACGAGCCTTAACCTGACGAGCCTTCA 176

DB 835 TGGCAACATTGGCTCTGCAATCGAATGAAACTTCAGGAGACCTAGCTACAGAGTATCTCA 894

OY 177 GCTA 180

DB 895 ACTA 898

Search completed: December 8, 2002, 18:33:58
Job time : 553.856 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:16:58 ; Search time 576.736 Seconds
(Without alignments)
7329.213 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atggcaatcctgacgctcac.....gtaattgagatcattcac 261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlcc:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_hlc:*
12: gb_estl3:*
13: gb_estl4:*
14: gb_estl5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95.8	36.7	659	AG107545	AG107545 Pan trogl
2	84.8	32.5	612	BH267783	BH267783 CH230-186
3	71	27.2	362	AV653073	AV653073 AV653073
4	38.6	14.8	198	BG197160	BG197160 RST16397
5	37	14.2	276	BG203357	BG203357 RST22738
6	37	14.2	277	BG184205	BG184205 RST3126 A

C	7	37	14.2	239	12	BG206497	BG206497 RST25946
C	8	35.8	13.7	697	17	AZ897813	AZ897813 RPCI-24-2
C	9	34.8	13.3	724	17	BH671765	BH671765 BOMKY36TR
C	10	34.2	13.1	463	12	BF930674	BF930674 MR2-NM013
C	11	34.2	13.1	536	14	BM892233	BM892233 sam57H07.
C	12	34.2	13.1	596	10	BE661877	BE661877 6-C8 Gmax
C	13	34	13.0	475	10	BE346444	BE346444 SP25104.Y
C	14	34	13.0	563	17	AF046628	AF046628 AF046628
C	15	34	13.0	631	17	AG132233	AG132233 Pan trogl
C	16	34	13.0	735	17	BH794645	BH794645 ME_MBA000
C	17	34	13.0	1027	14	BQ050697	BQ050697 AGENCOURT
C	18	33.8	13.0	284	17	AL768846	AL768846 Arabidops
C	19	33.8	13.0	321	12	BG212237	BG212237 RST31821
C	20	33.6	12.9	530	9	AA310614	AA310614 EST18161
C	21	33.2	12.7	853	17	BH314331	BH314331 CH230-99C
C	22	33.2	12.7	865	17	AZ550383	AZ550383 ENTER44TR
C	23	32.8	12.6	407	10	AW750032	AW750032 PM2-BT054
C	24	32.8	12.6	561	10	AV979271	AV979271 ATR10R11
C	25	32.6	12.5	426	13	BM434433	BM434433 HS-5118-B
C	26	32.4	12.4	435	17	AQ462091	AQ462091 HS-5118-B
C	27	32.4	12.4	823	17	CNS05RMX	CNS05RMX Tetraodon
C	28	32.2	12.3	771	17	AZ724950	AZ724950 RPCI-24-6
C	29	32	12.3	533	10	BE070217	BE070217 OVA-BT040
C	30	32	12.3	661	14	BQ839707	BQ839707 B15 Chick
C	31	32	12.3	819	17	BH419036	BH419036 BOCYMW5TR
C	32	32	12.3	912	12	BE683775	BE683775 BOCYMW5TR
C	33	32	12.3	930	17	BH150843	BH150843 ENT0139TR
C	34	31.8	12.2	428	9	AU226504	AU226504 BOMT140TR
C	35	31.8	12.2	640	10	BS589964	BS589964 BOMOT38TR
C	36	31.8	12.2	839	17	CNS02TGO	CNS02TGO Tetraodon
C	37	31.8	12.2	841	17	BF030090	BF030090 601557176
C	38	31.8	12.2	915	17	AZ684294	AZ684294 ENUGU94TR
C	39	31.8	12.2	966	17	CNS03AZE	CNS03AZE Tetraodon
C	40	31.6	12.1	426	17	AO523546	AO523546 HS-5207_A
C	41	31.6	12.1	451	13	BJ445420	BJ445420 BJ445420
C	42	31.6	12.1	552	17	BH741726	BH741726 g136g03.g
C	43	31.6	12.1	552	17	BH725020	BH725020 BOMB11TR
C	44	31.6	12.1	642	17	BH725020	BH725020 BOMB11TR
C	45	31.6	12.1	800	17	BH672114	BH672114 BOMOT38TR

ALIGNMENTS

RESULT 1
AG107545 659 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
LOCUS
AG107545
ACCESSION
AG107545.1 GI:16728063
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes male lymphoblast DNA, clone: lib:PTB Chimpanzee Male
BAC library clone: PTB-112G09.F.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE
BAC end sequences of library PTB
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE
Direct Submission
JOURNAL
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Saitama-shi, Tsukuba-shi, Ibaraki-shi, Japan
1-7-22 Saitama-shi, Tsukuba-shi, Ibaraki-shi, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
COMMENT
Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the Kd process and may have higher chance of
clone tracking errors.

PRIMERS
Sequencing: -21M13
LIBRARY
Vector : PK5145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. .659
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/db_xref="taxon:9598"
/clone="PTB-112G09.F"
/sex="male"
/cell_type="lymphoblast"
/clone_id="PTB Chimpanzee Male BAC Library"
BASE COUNT 181 a 168 c 121 g 189 t
ORIGIN

Query Match 36.7% Score 95.8; DB 17; Length 659;
Best Local Similarity 71.1% Pred. No. 5.1e-21;
Matches 143; Conservative 0; Mismatches 52; Indels 6; Gaps 1;
QY 43 ATACCATCATATTCCTCAGGCTCATATAAAGAGCTCTTCTTCTTGGAAACATGACCA 102
DB 388 ATGCTCTCTCTCTCCACAGGTTCCATTAAGTGAAGTCTCTCTCTTGGTACCATGATCGG 447
QY 103 GATTGGGCAACGCTCTCCATCATGCTTTCAGCAAGGAAACCTAAGAGTCA-----AA 156
DB 448 GGTGGGCAAGATCTCCACATGATCTTTAGCAATGGAACCTAATAGTTAATCAGGAT 507
QY 157 GGCATTTATTTACCGGAATGCGGACATTTGCTCTGACATCGGTTACCTCAGCAGCCCTA 216
DB 508 GCGTTTATTAACCTGATGATGCCAATCTTGTCTTGGACATCATGAACCTTCAGAGACCTA 567
QY 217 ACCTTCGACGACCTTCAGCTA 237
DB 568 GCTACAGAAATATCTTCACTA 588

RESULT 2
BH267783/C 612 bp DNA linear GSS 30-NOV-2001
LOCUS BH267783
DEFINITION CH230-186C1.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH267783
VERSION BH267783.1 GI:17180093
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 612)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
A., Gebregregis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSs: CH230-186C1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@igmr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: T7

FEATURES
Class: BAC ends.
Location/Qualifiers
source
1. .612
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/strain="BN/SSNhd/KCw"
/db_xref="taxon:10116"
/clone="CH230-186C1"
/clone_id="CHORI-230 Segment 1"
/sex="Female"
/note="Vector: pTARAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNhd/KCw) BAC library produced by
Pieter de Jong"
BASE COUNT 168 a 145 c 133 g 166 t
ORIGIN

Query Match 32.5% Score 84.8; DB 17; Length 612;
Best Local Similarity 69.5% Pred. No. 1.6e-17;
Matches 132; Conservative 0; Mismatches 52; Indels 6; Gaps 1;
QY 53 TATCCATGAGGCTCATATAAAGAGCTCTTCTTCTTGGAAACATGACCAAGTTGGCAA 112
DB 603 TCTCTAGGCTCCATTAAGTGAAGTCTCTCTTGTACCATGATGAGGCTGGGCA 544
QY 113 ACGTCTCCACATGACTTTCAGCAAGGAAACCTAAGAGTCA-----AAGCATTTATT 166
DB 543 AGATCTCTTAACATGACCTTAAAGCAACGAAACCTAAGGTTAACCAAGATGCTTCTATT 484
QY 167 ACCGGAATGCCGACATTTGCTCTGACATCGGCTTACCTCAGCAGGCTTACTGACG 226
DB 483 ACCTTACGCGCAACATTTGCTTTCAGCATCATGAACCTCAGGAGCGTACCTCGGACT 424
QY 227 ACCTTACGCT 236
DB 423 ATCTTCAGCT 414

RESULT 3
AV653073 362 bp mRNA linear EST 15-JAN-2002
LOCUS AV653073
DEFINITION AV653073 GLC Homo sapiens cDNA clone G1CDB01.3, mRNA sequence.
ACCESSION AV653073
VERSION AV653073.1 GI:9874087
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 362)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Gu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
Location/Qualifiers
source
1. .362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="G1CDB01"
/clone_id="GLC"
/tissue_type="corresponding non cancerous liver tissue"

```

/dev-stage="Adult"
/lab_host="SOLR"
/Note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      102 a      80 c      78 g      100 t      2 others
ORIGIN
Query Match      27.2%; Score 71; DB 10; Length 362;
Best Local Similarity 75.4%; Pred. No. 5.6e-13;
Matches 101; Conservative 0; Mismatches 31; Indels 2; Gaps 1;

OY 4 GCAATCTGACGCTCAACGCTTCTGTTGTTATTAATACCATCATATCCATGAG 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 228 GCAAGCTTGAAGCTCAGCTTTGCTCATCTCATATTATTAATGACGACCATCCATCTG 287
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 64 GCT--CATTAAGAGCTTTCTTCTTGAAACATGACCAAGATTGGGCAACGTCCTCCA 121
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 288 GTTCCCATTAAGTGAGTGTGCTCTGTGTCACATGATCGNGTTGGGCAAGATCTCCA 347
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 122 ACATGACTTTCAGC 135
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 348 ACATGACTTTTACG 361
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 4
Bg197160/c      198 bp      mRNA      linear      EST 21-APR-2001
LOCUS          Bg197160
DEFINITION     RST16397 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION      Bg197160
VERSION         Bg197160.1 GI:13718847
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 198)
AUTHORS        Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
                Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
                Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
                ,E., Veloso,N., Kliska,A., Hess,J., Colhren,K., Lo,K., Offenbacher
                ,J., Danzig,J. and Ducar,M.
                Creation of genome-wide protein expression libraries using random
                activation of gene expression
                Nat. Biotechnol. 19 (5), 440-445 (2001)
                21227151
TITLE          Creation of genome-wide protein expression libraries using random
                activation of gene expression
JOURNAL        Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE        21227151
COMMENT        Contact: Scott J. Cain
                Athersys, Inc.
                3201 Carnegie Ave, Cleveland, OH 44115, USA
                Tel: 216 431 9900
                Fax: 216 361 9596
                Email: scai@atersys.com
                High quality sequence stop: 148.
                Location/Qualifiers
FEATURES       source
               1..198
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="Athersys RAGE Library"
               /cell_line="HT1080"
               /note="See 'Creation of Genome-wide Protein Expression
               Libraries using Random Activation of Gene Expression',
               Nature Biotechnology, in press. Note that even though the
               Nature Biotechnology, in press. Note that even though the
               cell type indicated is HT1080, since a random activation
               method was used, these sequence tags are not necessarily
               expressed in HT1080 under normal circumstances."
BASE COUNT      55 a      56 c      41 g      46 t
ORIGIN
Query Match      14.8%; Score 38.6; DB 12; Length 198;
Best Local Similarity 77.0%; Pred. No. 0.038;
Matches 47; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 4 GCAATCTGACGCTCAACGCTTCTGTTGTTATTAATACCATCATATCCATGAG 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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```

Db 116 GCAAGCTTGAAGCTCAGCTTTGCTCATCTCATATTATTAATGACGACCATCCATG 57
OY 64 G 64
Db 56 G 56

RESULT 5
Bg203357/c      276 bp      mRNA      linear      EST 21-APR-2001
LOCUS          Bg203357
DEFINITION     RST27238 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION      Bg203357
VERSION         Bg203357.1 GI:13725044
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 276)
AUTHORS        Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
                Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
                Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
                ,E., Veloso,N., Kliska,A., Hess,J., Colhren,K., Lo,K., Offenbacher
                ,J., Danzig,J. and Ducar,M.
                Creation of genome-wide protein expression libraries using random
                activation of gene expression
                Nat. Biotechnol. 19 (5), 440-445 (2001)
                21227151
TITLE          Creation of genome-wide protein expression libraries using random
                activation of gene expression
JOURNAL        Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE        21227151
COMMENT        Contact: Scott J. Cain
                Athersys, Inc.
                3201 Carnegie Ave, Cleveland, OH 44115, USA
                Tel: 216 431 9900
                Fax: 216 361 9596
                Email: scai@atersys.com
                High quality sequence stop: 276.
                Location/Qualifiers
FEATURES       source
               1..276
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="Athersys RAGE Library"
               /cell_line="HT1080"
               /note="See 'Creation of Genome-wide Protein Expression
               Libraries using Random Activation of Gene Expression',
               Nature Biotechnology, in press. Note that even though the
               Nature Biotechnology, in press. Note that even though the
               cell type indicated is HT1080, since a random activation
               method was used, these sequence tags are not necessarily
               expressed in HT1080 under normal circumstances."
BASE COUNT      92 a      51 c      59 g      74 t
ORIGIN
Query Match      14.2%; Score 37; DB 12; Length 276;
Best Local Similarity 75.4%; Pred. No. 0.15;
Matches 46; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4 GCAATCTGACGCTCAACGCTTCTGTTGTTATTAATACCATCATATCCATGAG 63
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 67 GCAAGCTTGAAGCTCAGCTTTGCTCATCTCATATTATTAATGACGACCATCCATG 8
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
OY 64 G 64
Db 7 G 7

RESULT 6
Bg184205/c      277 bp      mRNA      linear      EST 21-APR-2001
LOCUS          Bg184205
DEFINITION     RST3126 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION      Bg184205
VERSION         Bg184205.1 GI:13705892
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 277)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,J., Daniels,J. and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaithersys.com

FEATURES
source location/Qualifiers
1..277
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 94 a 51 c 58 g 74 t
ORIGIN

Query Match 14.2% Score 37; DB 12; Length 277;
Best Local Similarity 75.4%; Pred. No. 0.15;
Matches 46; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 4 GCAATCCTGACGCTCAGCTTCAATCTGTTATTAATCAATATCCATGAG 63
Db 68 GCAAGCTTGAGCTCAGCTTTGCTCATCTCATTAATGCGACGACATCCATCTG 9
QY 64 G 64
Db 8 G 8

RESULT 7
BG206497/c 299 bp mRNA linear EST 21-Apr-2001
LOCUS RST25946 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG206497
ACCESSION BG206497.1 GI:13728184
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 299)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,J., Daniels,J. and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaithersys.com

FEATURES
source location/Qualifiers
1..299
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 98 a 56 c 65 g 80 t
ORIGIN

Query Match 14.2% Score 37; DB 12; Length 299;
Best Local Similarity 75.4%; Pred. No. 0.16;
Matches 46; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 4 GCAATCCTGACGCTCAGCTTCAATCTGTTATTAATCAATATCCATGAG 63
Db 90 GCAAGCTTGAGCTCAGCTTTGCTCATCTCATTAATGCGACGACATCCATCTG 31
QY 64 G 64
Db 30 G 30

RESULT 8
A2897813 697 bp DNA linear GSS 05-MAR-2001
LOCUS RPCI-24-210N16.TJ RPCI-24 Mus musculus genomic clone RPCI-24-210N16
DEFINITION A2897813
ACCESSION A2897813
VERSION A2897813.1 GI:13216758
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 697)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Zhao,S., Nieman,W., Malek,J., Shatsman,S., Akintel,B., Levins,M., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other-GSSs: RPCI-24-210N16.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

CLONES are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@tigr.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end plates: 210 /row: N column: 16
Seq primer: SP6
Class: BAC ends.
FEATURES
source location/Qualifiers
1..697
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-210N16"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pTRABAC1; Site_1: BamHI; Site_2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTABlacI cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA.

BASE COUNT 178 a 183 c 167 g 169 t

Query Match 13.7%; Score 35.8; DB 17; Length 697;
Best Local Similarity 57.7%; Pred. No. 0.59;
Matches 64; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 3 GGCATTCCTACCTCAGCTTCATCATCTGTTATTAATACCATATATCCATGA 62
DB 557 GGCGTTCACACCTCTCTCTGCTACCAATTTGCTAAGAAATCCACCAATCCAGGA 616
QY 63 GGCCTATTAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAA 113
DB 617 AGCCTCGGGAAGGCTCTGACTCTCCCGAGTGAACACTCTGGGCGA 667

RESULT 9
BH671765/c 724 bp DNA linear GSS 19-FEB-2002
LOCUS BOMKY36TR BO_2_3_KB Brassica oleracea genomic clone BOMKY36, DNA
DEFINITION sequence.
ACCESSION BH671765
VERSION BH671765.1 GI:18736884
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 724)
Town, C.D., Van Aken, S., Utenback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
JOURNAL Contact: Chris Town
COMMENT TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source 1..724
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMKY36"
/note="Vector: PHOSI; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOSI using BstXI linkers"

BASE COUNT 226 a 144 c 162 g 192 t

Query Match 13.3%; Score 34.8; DB 17; Length 724;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 87; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 48 ATCAATTCCTAGAGGCTCATTAAGAGTCTTCTTGTGAACATGACCAAGATTG 107
DB 698 ATTAGATTACAGATGAAGATTAATGAAATATCCAAACCTTAACCTCACTAATTA 639
QY 108 GCGAAGCTCTCCACATGATCTTTCAGCAACGAAACTAAGATCAAGCAATTTATTA 167
DB 638 GGAATCTCTAATACATTAATAGAAATTCATCTACTAGAAAGGAAAGGTTT 579
QY 168 CCGAATGCCGACATTTGCTCGACATCGCGTAACCTCAGCAGGCTTACTCT 221
DB 578 CATTTCCTCAAGCTTTGGTGCCCTTCTCTCTCTGTAAGTGGGCTCTCTCT 525

RESULT 10
BF930674 463 bp mRNA linear EST 22-JAN-2001
LOCUS MR2-NT0135-131200-014-g01 NT0135 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF930674
ACCESSION BF930674.1 GI:12347907
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 463)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bioness, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/TIGR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?PL=MR2&L=MR2-NT0135-131200-014-g01&L3=2000-12-13&L4=1)
Seq primer: puc 18 forward
High quality sequence stop: 462.

FEATURES
source 1..463
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0135"
/dev_stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESNES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 156 a 97 c 115 g 95 t

Query Match 13.1%; Score 34.2; DB 12; Length 463;
Best Local Similarity 54.3%; Pred. No. 1.7;
Matches 69; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 35 TGTATTATATACATCAATATCCATGAGGCTCATTAAGAGTCTTCTTGTGAAC 94
DB 41 TGCATTTGTAGAGGCTGACGACACAGAGTGAACAGCAAGAGGCTTCTTGAAC 100
QY 95 ATGACCAAGATTTGGGCAACGCTCCCAACATGACTTTCAGCAAGGAAACTAAGATCA 154
DB 101 ATAACCGAATGGAAGAGCTTGCAGCATCAAGAAATTCGAGATTAAGACCA 160
QY 155 AAGCAT 161
DB 161 ACAGCTT 167

RESULT 11
BM892233/c

DEFINITION sam51h07.y1 Gm-cl1069 glycine bp mRNA linear EST 11-MR-2002
Gm-cl1069.1805 5' similar to TR:O9Z0E5 O9Z0E5 F9013.24 PROTEIN. ;
RNA sequence.
R8493233

ACCESSION	BM892233
VERSION	BM892233.1
KEYWORDS	GI:19347353
SOURCE	EST.
ORGANISM	soybean.

ORGANISMISM
Glycine max
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicts;
Rosidae; eutroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
glycine.
1 (bases 1 to 536)
Shoenaker, R., Keim, P., Vodkin, L., Frenkel, I., Guss, D., et al.
REFERENCE
AUTHORS

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 536)	Shoemaker, R., Keim, P., Vodka, L., Erpelding, J., Cornell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shah, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	Public Soybean EST Project	Unpublished (1999)	Contact: Shoemaker R./Public Soybean EST Project

Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 Or contact: ccul@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 421.

```

FEATURES
source      Location/Qualifiers
1. .536

```

```

BASE COUNT      123 a      122 g      181 t
ORIGIN
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1069-3805"
/clone_lib="Gm-c1069"
/tissue_type="degenerating cotyledons, 9-10 day old
etiolated seedling"
/lab_host="DH10b"
/note="Vector: pBluescript II SK+; Site:1: EcoRI; Site:2:
XhoI. The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10 host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

```

[illegible]

Db 149 AGAACACAGATCAACGAATTCTTGTAACAGG 119

RESULT 12	596 bp	mrna	linear	EST 06-SEP-2000
BE661877/c				
LOCUS				
DEFINITION	BE661877			
ACCESSION	6-C8 Gmasc	Glycine max	cdna, mRNA	sequence.
VERSION	BE661877			
KEYWORDS	BE661877.1	GI:9987769		
EST.				
SOURCE				
ORGANISM	soybean.			

ORGANISM
Glycine max
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine
1 (bases 1 to 596)
Harris,N., Chapman,B.P. and Gijzen,M.
Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M

Agriculture and Agri-Food Canada
 1391 Sandford Street, London, Ontario, Canada N5V 4R7
 Tel: 519 457 1470
 Fax: 519 457 3997
 Email: glizem@agr.ca
 Location/Qualifiers
 1..596

BASE COUNT
ORIGIN

143 a 139 c 131 g 179 t 4 others

```

/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="Gmax8C"
/tissue_type="Seed coats"
/lab_host="E. coli strain XL0R"
/note="Vector: pBK-CMV; Site.1: EcoRI; Site.2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from green seed coats in mid to late developmental stages
, average fresh weight 250 mg per seed. Rates of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adaptors were ligated to the
blunt-ended cDNA fragments and the products were digested
with XhoI for directional cloning into lambda ZAP Express
vector. This lambda library was amplified once using E.
coli host strain XL1 Blue MRF+. Inserts were then
subcloned by mass excision using Exsist helper phage for
conversion into phagemid vector pBK-CMV in E. coli host
strain XL0R."

```

Query Match	Best Local Similarity	13.18;	Score 34.2;	DB 10;	Length 596;
Matches	78; Conservative	51.78;	Pred. No. 1.9;	Mismatches 0;	Indels 73; Gaps 0;
QY	21 CCTCAACATCATCTTGTTATTATATACATCAATATCCCATGAGGCTCTATAAACGAGTCT				
Db	498 CCTAGTCTCAGAGCTCCGAATTAAGTTCTATCAAGAACCAATAATGGCAATGGCATGGCACT				
QY	81 TTCTCTCTTGAACATATACCAAGATTGGGCAACGCTCCAACTGACTTTCAGCAAGG				
Db	438 TTATATACGGAAGAGCTGATGATATATGGGCAACCAACAAACGGAATTCACCTTCAAGA				
QY	141 AAAACTAGAGTCAAAAGGCATTTATTACCGG				
Db	378 AGAACACAGATCAACCAATTTCTGTAAACAGG				

RESULT 13	BE346444/c	LOCUS	DEFINITION	475 bp	max	CDNA	clone	GENOME	SYSTEMS	CLONE ID:
	BE346444									
	SP25T04.y1		Gm-cl042	Glycine	max					
				bp						
				mrna						
				linear						
				EST	04-DEC-2001					

Gm-cl042-1592.5' similar to TR:Q9ZOE5 Q9ZOE5 F9013.24 PROTEIN. ;
 mRNA sequence.
 BE346444
 BE346444.1 GI:9258297
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Glycine max
 soybean.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 475)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 R., Ritter, E., Korn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccutresgen.com
 High quality sequence stop: 475.
 Location/Qualifiers
 1..475
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl042-1592"
 /clone_1lb="Gm-cl042"
 /rissue_type="whole seedling without cotyledons"
 /lab_host="DH10B"
 /note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from 2 week old seedlings with the cotyledons removed at
 the time of harvest. The seedlings for the cultivar Ralden
 were grown in a growth chamber using germination paper.
 Complementary DNA was synthesized from mRNA using a primer
 consisting of a poly(dT) sequence with a XhoI restriction
 site. EcoRI adapters were ligated to the blunt-ended cDNA
 fragments followed by XhoI digestion. The cDNA fragments
 were directionally cloned into the EcoRI-XhoI restriction
 site of the phuscript vector. The ligated cDNA fragments
 were transformed into DH10B host cells (Gibco BRL). This
 library was constructed by Dr. Randy Shoemaker."
 BASE COUNT 103 a 100 c 102 g 170 t
 ORIGIN
 Query Match 13.0%; Score 34; DB 10; Length 475;
 Best Local Similarity 53.8%; Pred. No. 2;
 Matches 70; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
 QY 21 CCTCACTCATCTGTTGTTATTAATACATATATCCATGAGCTCATTAAGAGCT 80
 DB 156 CCTAGTCTTAGCTCCTCAATATGTTCAAGAGCAAAATGCAATGGCATGGCACT 97
 QY 81 TTCTCTTGGAACATGAGCAAGATTGGCAAACTCTCCACATGACTTTGAGCAAG 140
 DB 96 TTCACTATGGAAGAGCTGAGATATATGGCAAAACAAAGGAATTCACCTCAAGA 37
 QY 141 AAACCTAGA 150
 DB 36 AGACACACA 27
 RESULT 14

AF046628 563 bp DNA linear GSS 02-NOV-2000
 LOCUS
 DEFINITION
 AF046628 Mus musculus 129Sv/Ev Mus musculus genomic clone OST1450,
 DNA sequence.
 AF046628
 AF046628.1 GI:3068691
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 563)
 Zambrowicz, B.P., Friedrich, G.A., Buxton, E.C., Lilleberg, S.L.,
 Persson, C. and Sands, A.T.
 Disruption and sequence identification of 2,000 genes in mouse
 embryonic stem cells
 Nature 392 (6676), 608-611 (1998)
 98219085
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 OmniBank Sequence Tag
 Class: exon-trapped.
 Location/Qualifiers
 1..563
 /organism="Mus musculus"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST1450"
 /clone_1lb="Mus musculus 129Sv/Ev"
 /cell_type="embryonic stem cell"
 BASE COUNT 150 a 118 c 119 g 137 t 39 others
 ORIGIN
 Query Match 13.0%; Score 34; DB 17; Length 563;
 Best Local Similarity 64.8%; Pred. No. 2.2;
 Matches 46; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 28 CTAATCTGTTATTAATACATATATCCATGAGCTCATTAAGAGCTTTCTTCT 87
 DB 115 CGCATCTGTTGTCGNNANNAATATGCTATGAGCTCATTAAGAGCTTACTTCA 174
 QY 88 TGAACATGA 98
 DB 175 TNAATAATATTA 185
 RESULT 15
 AG132233/c 631 bp DNA linear GSS 04-NOV-2001
 LOCUS
 DEFINITION
 AG132233 Pan troglodytes DNA, clone: PTB-144117.F, genomic survey sequence.
 AG132233
 AG132233.1 GI:16661911
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male
 BAC library clone:PTB-144117.F.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library PTB
 Unpublished
 2 (bases 1 to 631)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suenhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

COMMENT

(E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB this BAC end
was generated during the Red process and may have higher chance of
clone tracking errors.

Sequencing: -21M13
LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

FEATURES

source

Location/Qualifiers

1..631

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="PTB-144117.F"

/sex="male"

/cell_type="lymphoblast"

BASE COUNT 181 a 148 c 98 g 202 t 2 others

ORIGIN

Query Match

Best Local Similarity 13.0%; Score 34; DB 17; Length 631;

Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 39 ATTAAATACATCAATATCCATGAGGCTCATAAACGAGCTTCTTCTTGAAACATGA 98

DB 233 ATTAAATATCTTTATTATTCATTTAATTAATCAATAAACAAGTCTATAAATGGAATGATGA 174

QY 99 CCAAGATTGGGCAACGCTCCAAACATGACTTCACGCAAGCAAAA 144

DB 173 TCNAACCTCGTGTAGAGGAATGTAACTTAGGAGAGTGAAA 128

Search completed: December 8, 2002, 19:27:07
Job time : 589.736 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:14 ; Search time 74.3192 Seconds
(without alignments)
7908.746 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746

Perfect score: 261
Sequence: 1 atcgcaatcctgaagctcag.....gttaattgagaatcattac 261

Scoring table: IDENTITY_NUC
Gap 10.0 , Gape 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_101002:.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251	96.2	1186	24	ABK33576
2	121.2	46.4	741	19	AAV69899
3	121.2	46.4	954	19	AAV69887
4	121.2	46.4	954	19	AAV41378
5	121.2	46.4	954	19	AAV41372
6	121.2	46.4	954	22	AAV41311
7	121.2	46.4	954	22	AAV41311
8	121.2	46.4	954	22	AAV41311
9	121.2	46.4	1945	24	ABK12877

10	121.2	46.4	2226	24	ABK12876
11	121.2	46.4	2271	19	AAZ9964
12	121.2	46.4	2274	19	AAV70285
13	121.2	46.4	2390	24	ABK40274
14	118	45.2	1823	20	AAK80223
15	102	39.1	957	22	AAK6481
16	95.6	36.6	735	19	AAV69898
17	95.6	36.6	951	19	AAV69900
18	95.6	36.6	951	21	AAV39156
19	95.6	36.6	951	21	AAZ9965
20	95.6	36.6	951	21	AAZ99024
21	95.6	36.6	1538	19	AAV69886
22	95.6	36.6	1574	22	AAH25526
23	95.6	36.6	1630	19	AAV41377
24	95.6	36.6	1630	19	AAV41371
25	95.6	36.6	1630	22	AAV41310
26	95.6	36.6	1630	22	AAV41310
27	95.6	36.6	1630	22	AAV41310
28	95.6	36.6	1630	22	AAV41310
29	95.6	36.6	1630	22	AAV41310
30	95.6	36.6	1630	22	AAV41310
31	95.6	36.6	1630	22	AAV41310
32	95.6	36.6	1630	22	AAV41310
33	91	34.9	522	22	AAV3369
34	81.6	31.3	2029	21	AAV39155
35	73.6	28.2	519	21	AAZ9968
36	73.6	28.2	519	21	AAZ9969
37	73.6	28.2	519	21	AAZ9972
38	73.6	28.2	546	21	AAZ99971
39	73.6	28.2	564	21	AAZ99967
40	73.6	28.2	564	21	AAZ99970
41	63	24.1	519	21	AAZ99973
42	36.2	13.9	2240	20	AAV18563
43	36.2	13.9	2291	20	AAV18564
44	36.2	13.9	3405	20	AAV18560
45	35.2	13.5	351	23	ABV23301

ALIGNMENTS

RESULT 1
ABK33576
ID ABK33576 standard; CDNA: 1186 BP.
XX
AC ABK33576;
XX
DT 08-MAY-2002 (first entry)
XX
DE CDNA encoding human PRO protein, Seq ID No 81.
KW Human: secreted protein; PRO: tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.

CDNA encoding huma
DNA encoding a hum
Human osteoprotege
CDNA encoding huma
Human TRANCE encod
Rat osteoclast dif
Nucleic acid encod
Nucleic acid sequenc
Mouse OBK nucleoti
DNA encoding a mur
Osteoclast formati
Nucleic acid encod
Nucleotide sequenc
NF-KB receptor act
NF-KB receptor act
Murine receptor ac
Murine receptor ac
Murine RANKL (reco
Nucleotide sequenc
Murine TRANCE enco
CDNA encoding mous
Human osteoprotege
DNA encoding a mur
Mouse OBK nucleoti
DNA encoding a syn
DNA encoding a syn
DNA encoding osteo
DNA encoding osteo
DNA encoding a syn
DNA encoding osteo
CDNA sequence SEO
CDNA sequence SEO
CDNA encoding CDNA.
Human prostate exp

Db 320 GTTCCCTAAAGTGTCTGCTTGTGTAACATGATCGGGGTTGGCCAAAGATCTCCA 379
 QY 122 ACATGACTTTCAGCAGCAAGAACTAAGAGTCA-----AAGCATTTTATTACCGGAATG 175
 Db 380 ACATGACTTTTAGAGAAAGAACTAAGTAAATAGTAAATCAGATGGCTTTATTACCTGTATG 439
 QY 176 CCGACATTTGCTCTCGACATCGCGTAACTCTGACAGACCTTTCAGC 235
 Db 440 CCAACATTTGCTTTCGACATCATGAACTTCAAGACCTAGCTACAGAGTATCTTCAAC 499
 QY 236 TA 237
 Db 500 TA 501
 RESULT 3
 AAV69887 standard: cDNA to mRNA: 954 BP.
 AC AAV69887;
 DT 10-FEB-1999 (first entry)
 DE Nucleic acid encoding a human OCIF-binding molecule (OBM).
 XX
 KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /*tag= a
 XX
 PN MO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 DR WPI: 1998-594563/50.
 DR P-PSDB; AAW63018.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PS Claim 38; Page 115; 151pp; Japanese.
 XX
 CC The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone

CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 SQ Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other:
 Query Match 46.4%; Score 121.2; DB 19; Length 954;
 Best Local Similarity 74.8%; Pred. No. 1.5e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCATCTGACGCTCAGCCTTCAACTCATCTTTATTATATACATCAATATCCATGAG 63
 Db 473 GCAAGCTGAAGCTCAGCCTTGTGCTCATCTCACTATTATATGCAAGCATCCCATGTG 532
 QY 64 GCT--CATAAAGAGAGTCTTCTTCTTGAACATGACCAAGATTGGGCAACGCTTCCA 121
 Db 533 GTTCCCTAAAGTGTGTCTGCTTGTGTAACATGATCGGGGTTGGCCAAAGATCTCCA 592
 QY 122 ACATGACTTTCAGCAGCAAGAACTAAGAGTCA-----AAGCATTTTATTACCGGAATG 175
 Db 593 ACATGACTTTTAGCAATGAAACTAATAGTAAATCAGAGATGCTTTATTACCTGTATG 652
 QY 176 CCGACATTTGCTCTCGACATCGCGTAACTCTGACAGACCTTTCAGC 235
 Db 653 CCAACATTTGCTTTCGACATCATGAACTTCAAGAGACCTAGCTACAGAGTATCTTCAAC 712
 QY 236 TA 237
 Db 713 TA 714
 RESULT 4
 AAV41378 standard: cDNA; 954 BP.
 ID AAV41378
 AC AAV41378;
 DT 08-OCT-1998 (first entry)
 DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 XX
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /*tag= a
 FT /product= "human RANKL (ligand for RANK)"
 XX
 PN MO9828426-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US23775.
 XX
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 DR WPI: 1998-377657/32.
 DR P-PSDB; AAW69957.
 XX
 PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells
 XX

XX Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 1..954
 FT CDS /tag= a
 FT /product= "Human RANK ligand (RANKL) protein"
 PN US6271349-B1.
 PD 07-AUG-2001.
 XX
 PF 17-DEC-1998; 98US-0215649.
 XX
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0772330.
 PR 07-MAR-1997; 97US-0813509.
 PR 22-DEC-1997; 97US-0996139.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Dougal1 WC, Galibert L;
 XX
 DR MPI: 2001-520313/57.
 DR P-PSDB; AAE08738.
 XX
 PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for
 PT regulating immune response, in screening for RANK inhibitors, or as an
 PT adjunct therapy for disease characterized by neoplastic cells that
 PT express RANK -
 XX
 PS Example 7; Column 69-71; 47pp; English.

SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;
 Query Match 46.4%; Score 121.2; DB 22; Length 954;
 Best Local Similarity 74.8%; Pred. No. 1.5e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCATCCTGACGCTCAGCCCTTCACTCATCTTGTATTATATACATCAATATCCATGAG 63
 DB 473 GCATGCTGAAAGCTCAGCCCTTTGCTCATCTCACTATTATATGACACGACATCCATCTG 532
 QY 64 GCT-CATAAAGAGAGCTTTCTTTGGAACATGACCAAGATTGGCAACGCTTCCA 121
 DB 533 GTTCCCATTAAGAGAGCTTCTCTGTTGATGATGATCGGGGTGGCCCAAGATCTCCA 592
 QY 122 ACATGACTTTCAGCAAGCAAGAACTAAGAGCA-----AAGGATTTATACCGGAATG 175
 DB 593 ACATGACTTTCAGCAAGCAAGAACTAAGATTAATGATGATGATGCTTTTATTAACCTGATG 652
 QY 176 CCGACATTTGCTCTCGCATCGGTAACTCAGCAGGCTTAACCTCAGGACCTTCAGC 235
 DB 653 CCAACATTTGCTCTTCGACATCATGAAACTTCAGGAGACCTAAGATATCTTCAAC 712
 QY 236 TA 237
 DB 713 TA 714
 XX
 RESULT 7
 AAD08715
 ID AAD08715 standard; cDNA; 954 BP.
 XX
 AC AAD08715;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human receptor activator of NF- χ B ligand (hRANKL) cDNA.
 XX
 KW Human: receptor activator of NF- χ B; RANK; tumour necrosis factor; TNF;
 KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response;
 KW chromosome 18q22.1; hRANKL; chromosome 19q14; transmembrane protein; ss.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT 1..954
 FT CDS /tag= a
 FT /product= "Human RANKL protein"
 FT
 PN US6242213-B1.
 PD 05-JUN-2001.
 XX
 PF 22-DEC-1997; 97US-0995659.
 XX
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Anderson DM;
 XX
 DR MPI: 2001-407216/43.
 DR P-PSDB; AAE04426.
 XX
 PT New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF- χ B
 PT receptor activator) of the receptor activator of NF- χ B (RANK) -
 XX
 PS Claim 2; Column 61-64; 43pp; English.
 XX
 CC The present invention relates to receptor activator of NF- χ B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to

CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumour necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
 CC The ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is human RANKL (hRANKL)
 CC cDNA.
 XX
 SO Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other:
 Query Match 46.4%; Score 121.2; DB 22; Length 954;
 Best Local Similarity 74.8%; Pred. No. 1.5e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 OY 4 GCAATCCTGACGCTCAGCTTCACATCATCTGTTATTATACATCAATATCCCATAG 63
 DB 473 GCAACCTTGAGCTCAGCTCTTTGGCTCATCTCACTATTAAAGCCACGACATCCCATCTG 532
 OY 64 GCT--CATAAACGAGTCTTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTCCA 121
 DB 533 GTTCCCATTAAGTGAAGTCTGTCTCTTGATCCATGATCGGGGTTGGGCCAAGATCTCA 592
 OY 122 ACATACCTTTCGCAACGGAACCTAAGAGTCA-----AAGCATTTATTACCGGAATG 175
 DB 593 ACATACCTTTCGCAATGGAACCTAATAGTAAATACAGATGAGCTTTATTACCTGATG 652
 OY 176 CCGACATTTGCTCTCGACATCGGTAACCTCAGAGGCTTAACCTCGAGACCTTCAGC 235
 DB 653 CCAACATTTGCTTTCGACATCATGAAACTTCAGAGACCTAGCTACAGAGTATCTTCAAC 712
 OY 236 TA 237
 DB 713 TA 714
 XX
 RESULT 8
 AAD05904 ID AAD05904 standard; cDNA; 954 BP.
 XX
 AC AAD05904:
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human full-length RANKL (receptor activator of NF-kappaB ligand) cDNA.
 XX
 KW Human: receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopetritic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; BP; cytostatic; chromosome 13q14;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1.954
 FT CDS /*tag= a
 FT /product= "Human full-length RANKL (receptor activator
 FT of NF-kappaB ligand) protein"
 FT
 FT
 FT
 XX WO200136637-A1.
 XX
 XX PD 25-MAY-2001.
 XX
 XX PE 14-NOV-2000; 2000WO-US31459.
 XX
 XX PR 17-NOV-1999; 99US-0442029.
 XX
 XX PA (IMMV) IMMUNEX CORP.
 XX
 XX PI Anderson DM, Hughes AE;

XX
 DR WPI: 2001-329222/34.
 DR P-PDSB; AAE01993.
 XX
 PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 XX
 PS Example 7; Page 75-76; 96pp; English.
 XX
 CC The present invention relates to a novel receptor, referred to as RANK
 CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
 CC (tumour necrosis factor) receptor superfamily. RANK is a Type I
 CC transmembrane protein that interacts with TNF receptor-associated
 CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
 CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
 CC of the transcription factor NF-kappaB, a ubiquitous transcription factor
 CC that is most extensively utilised in cells of the immune system.
 CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
 CC negative effects of inflammatory reactions, and the effects of excess
 CC bone resorption. The RANK DNAs, proteins and their analogues are useful
 CC for the preparation of pharmaceutical compositions, for infecting target
 CC cells for use in gene therapy applications in diagnosing diseases
 CC associated with RANK, and as targets for use in screening assays. They
 CC may be used in the treatment or diagnosis of immune system dysfunction.
 CC The present invention also encompasses gene therapy methods to correct
 CC gene-activating mutations, associated with e.g. familial expansile
 CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 CC present sequence is a cDNA encoding full-length human RANKL (hRANKL).
 CC protein. The RANKL gene is located in chromosome 13q14.
 XX
 SO Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other:
 Query Match 46.4%; Score 121.2; DB 22; Length 954;
 Best Local Similarity 74.8%; Pred. No. 1.5e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 OY 4 GCAATCCTGACGCTCAGCTTCACATCATCTGTTATTATACATCAATATCCCATAG 63
 DB 473 GCAACCTTGAGCTCAGCTCTTTGGCTCATCTCACTATTAAAGCCACGACATCCCATCTG 532
 OY 64 GCT--CATAAACGAGTCTTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTCCA 121
 DB 533 GTTCCCATTAAGTGAAGTCTGTCTCTTGATCCATGATCGGGGTTGGGCCAAGATCTCA 592
 OY 122 ACATACCTTTCGCAACGGAACCTAAGAGTCA-----AAGCATTTATTACCGGAATG 175
 DB 593 ACATACCTTTCGCAATGGAACCTAATAGTAAATACAGATGAGCTTTATTACCTGATG 652
 OY 176 CCGACATTTGCTCTCGACATCGGTAACCTCAGAGGCTTAACCTCGAGACCTTCAGC 235
 DB 653 CCAACATTTGCTTTCGACATCATGAAACTTCAGAGACCTAGCTACAGAGTATCTTCAAC 712
 OY 236 TA 237
 DB 713 TA 714
 XX
 RESULT 9
 ABK12877 ID ABK12877 standard; cDNA; 1945 BP.
 XX
 AC ABK12877:
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE cDNA encoding human TRANCE protein splice variant 2.
 XX
 XX KW Human: tumour necrosis factor-related activation induced cytokine;
 KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
 KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
 KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
 KW exostosis; bursitis; multiple osteocartilaginous exostosis; chondrocyte;
 KW cartilage growth; skeletal growth; gene; ss.

XX	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FT	misc-feature 81..131
FT	/tag= a
FT	/note= "Tumour necrosis factor (ligand) superfamily,
FT	member 11 (TNFSF11), Specifically claimed in
FT	claim 4"
FT	misc-feature 81..140 b
FT	/tag= /note= "Target region for antisense nucleic acid"
FT	CDS 95..829
FT	/tag= c
FT	/product= "Human TRANCE (tumour necrosis factor-related
FT	activation induced cytokine) protein,
FT	splice variant 2"
XX	
PN	WO200216551-A2.
XX	
PD	28-FEB-2002.
XX	
PF	20-AUG-2001; 2001MO-US26101.
XX	
PR	18-AUG-2000; 2000US-226197P.
XX	
PA	(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX	
PI	Choi Y, Odgren PR, Marks SC:
XX	
DR	WPI: 2002-304119/34.
DR	P-PDSB; AAU78286.
PT	Treating mammal having disorder characterised by abnormal
PT	cartilage/skeletal growth such as dwarfism, acromegaly, by
PT	administering tumour necrosis factor-related activation induced
PT	cytokine-modulating agent to mammal -
XX	
XX	Disclosure; Fig 3; 55bp; English.
PS	
XX	The present invention relates to a new method of treating a mammal
CC	having a disorder comprising insufficient or excessive cartilage or
CC	skeletal growth. The method of the invention involves administering to
CC	the mammal a tumour necrosis factor-related activation induced cytokine
CC	(TRANCE)-modulating agent. The method is useful for treating a mammal
CC	having a disorder comprising insufficient or excessive cartilage or
CC	skeletal growth, where the disorder comprising insufficient cartilage
CC	or skeletal growth is selected from dwarfism, osteopetrosis,
CC	craniofacial-skeletal discrepancies and bone or cartilage damage
CC	resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
CC	arthritis, and disorders comprising excessive cartilage or skeletal
CC	growth are selected from acromegaly, gigantism, exostosis, cartilagene,
CC	exostosis bursata and multiple osteochondilaginous exostoses. The method
CC	is useful for inhibiting chondrocyte differentiation. The present
CC	nucleic acid sequence encodes the human TRANCE protein, splice variant
CC	2, of the invention. TRANCE is a member of the tumour necrosis factor
CC	family and acts directly on cartilage-producing cells (chondrocytes).
XX	
SQ	Sequence 1945 BP; 623 A; 326 C; 392 G; 601 T; 3 other:
	Query Match 46.4%; Score 121.2; DB 24; Length 1945;
	Best Local Similarity 74.8%; Pred. No. 2e-30;
	Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps
OY	
	4 GCATTCGAGCGCTTAGCCTTCAACTCTTGTTATTAAATACCATCATATCCCATGAG 63
DB	GGAAGCTGGAAAGCTAGCGCTTTGTGCATCTCATTAATTAATGCCACCGCATCCCATCTG 407
OY	
	64 GCT--CATAAAACGAGCTCTTCTCTTGGAAACATGACCACGATTGGGCAACGCTCCA 121
DB	GTTCCCATTAATAATAGTAGTGTCTCTTGTGTACCATGATGGGGGTTGGGCAAGATCTCCA 467
OY	
	122 ACATGACTTTACGCAACGGAACAACCTAAGAAGTCA-----AAGCATTTTATTCGGGATG 175

Db	468	ACATGACCTTTGTCGACATGGAACCTAATAGTATATCAGAGATGCTTTATTAACCTGATG	527
Oy	176	CCGACATTTGCTCTCGACATCGCGTAACTCAGACAGCCCTTAACCTGAGACCTTCAGC	235
Db	528	CCAAATATTGGCTTCGACATCATCAATAACCTTCAGAGAGACCTTAAGAGATATCTTCACG	587
Oy	236	TA 237	
Db	588	TA 589	
RESULT 10			
ABK12876			
ID	ABK12876	standard; cDNA; 2226 BP.	
XX	ABK12876;		
XX	18-JUN-2002	(first entry)	
XX	CDNA	encoding human TRANCE protein splice variant 1.	
DE			
XX			
KM	Human; tumour necrosis factor-related activation induced cytokine;		
KM	TRANCE; dwarfism; osteopetrosis; craniofacial/skeletal dyscrasy;		
KM	bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis		
KM	rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;		
KM	exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;		
KM	cartilage growth; skeletal growth; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	misc-feature	141..190	
FT		/tag= a	
FT		/note= "Tumour necrosis factor (ligand) superfamily,	
FT		member 11 (TNFSF11), target region for antisense	
FT		nucleic acid. Specifically claimed in claim 4"	
FT	CDS	157..1110	
FT		/tag= D	
FT		/product= "Human TRANCE (tumour necrosis factor-related	
FT		activation induced cytokine) protein,	
FT		splice variant 1"	
XX			
PN	WO200216551-A2.		
XX			
PD	28-FEB-2002.		
XX			
PF	20-AUG-2001; 2001WO-US26101.		
XX			
PR	18-AUG-2000; 2000US-22617P.		
XX			
PA	(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.		
XX			
PI	Choi Y, Odgren PR, Marks SC;		
XX			
DR	WPI; 2002-304119/34.		
DR	P-PSDB; AAN78285.		
XX			
PT	Treating mammal having disorder characterised by abnormal		
PT	cartilage/skeletal growth such as dwarfism, acromegaly, by		
PT	administering tumour necrosis factor-related activation induced		
PT	cytokine-modulating agent to mammal -		
XX			
PS	Disclosure; Fig 1; 55pp; English.		
XX			
CC	The present invention relates to a new method of treating a mammal		
CC	having a disorder comprising insufficient or excessive cartilage or		
CC	skeletal growth. The method of the invention involves administering to		
CC	the mammal a tumour necrosis factor-related activation induced cytokine		
CC	(TRANCE)-modulating agent. The method is useful for treating a mammal		
CC	having a disorder comprising insufficient or excessive cartilage or		
CC	skeletal growth, where the disorder comprising insufficient cartilage		
CC	or skeletal growth is selected from dwarfism, osteopetrosis,		

CC craniofacial-skeletal discrepancies and bone or cartilage damage
 CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
 CC arthritis, and disorders comprising excessive cartilage or skeletal
 CC growth are selected from acromegaly, gigantism, exostosis, catlaglinea,
 CC exostosis bursata and multiple osteocartilaginous exostoses. The method
 CC is useful for inhibiting chondrocyte differentiation. The present
 CC nucleic acid sequence encodes the human TRANCE protein, splice variant
 CC 1, of the invention. TRANCE is a member of the tumour necrosis factor
 CC family and acts directly on cartilage-producing cells (chondrocytes).
 CC
 S0 Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;

Query Match 46.4%; Score 121.2; DB 24; Length 2226;
 Best Local Similarity 74.8%; Pred. No. 2.1e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACGCTTCAAGCTTCACTGTTTATTAATACCATCATATCCCATGAG 63
 DB 629 GCAAGCTTGAAAGCTGAGCTTTTGGTCATCTCATTTATATGCCACCATCCATCTG 688
 QY 64 GCT--CATAAACAGAGTCTTCTTCTTGGAAACATGACCAAGATGGGCAAGCTCCCA 121
 DB 689 GTTCCCATTAATAGTGTCTCTCTTGTACCATATGCGGCTTGGCCAAAGATCTCCA 748
 QY 122 ACATGACTTTTCAGCAACGGAATAAGATCA-----AAGCATTTATTCAGGATG 175
 DB 749 ACATGACTTTTAGCAATGGAATAAGATTAATCAGATGGCTTTTATTAATCTGTATG 808
 QY 176 CCGACATTTGCTTCGACATCGGCTTAACCTCAGCAGGCTTAACCTGACAGACCTTCAGC 235
 DB 809 CCACCATTTGCTTCGACATCATGAAATTCAGAGACCTAGCTACAGATATCTTCAAC 868
 QY 236 TA 237
 DB 869 TA 870

RESULT 11
 AA299964
 ID AA299964 standard; DNA; 2271 BP.

AA299964;
 25-JUL-2000 (first entry)

XX DNA encoding a human osteoprotegerin ligand (OPGL).

XX
 DE Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 XX tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption; ss.

XX Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT CDS 185..1138
 FT /*tag= a
 FT /product= "osteoprotegerin ligand"

PN W0200015807-A1.

XX 23-MAR-2000.

PF 13-SEP-1999; 99MO-DK00481.

PR 15-SEP-1998; 98DK-0001164.
 PR 02-OCT-1998; 98OS-0102896.

PA (MEBI-) M & E BIOTECH AS.

PI Halkier T, Haaning J;

XX WPI; 2000-271444/23.

DR P-PSDB; AAV84417.

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -
 PS Disclosure; Page 75-77; 110pp; English.

XX
 CC The present sequence encodes a human osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 XX
 S0 Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;

Query Match 46.4%; Score 121.2; DB 21; Length 2271;
 Best Local Similarity 74.8%; Pred. No. 2.1e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACGCTTCAAGCTTCACTGTTTATTAATACCATCATATCCCATGAG 63
 DB 657 GCAAGCTTGAAAGCTGAGCTTTTGGTCATCTCATTTATATCCACCATCCATCTG 716
 QY 64 GCT--CATAAACAGAGTCTTCTTCTTGGAAACATGACCAAGTTGGCAAGCTTCGA 121
 DB 717 GTTCCCATTAATAGTGTCTCTCTTGTACCATATGCGGCTTGGCCAAAGATCTCCA 776
 QY 122 ACATGACTTTTCAGCAACGGAATAAGATCA-----AAGCATTTATTCAGGATG 175
 DB 777 ACATGACTTTTAGCAATGGAATAAGATTAATCAGATGGCTTTTATTAATCTGTATG 836
 QY 176 CCGACATTTGCTTCGACATCGGCTTAACCTCAGCAGGCTTAACCTGACAGACCTTCAGC 235
 DB 837 CCACCATTTGCTTCGACATCATGAAATTCAGAGACCTAGCTACAGATATCTTCAAC 896
 QY 236 TA 237
 DB 897 TA 898

RESULT 12
 AAV70285
 ID AAV70285 standard; DNA; 2274 BP.

AAV70285;

11-FEB-1999 (first entry)

XX Human osteoprotegerin binding protein from the pcDNA3/nuOPGp1.insert.

XX Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODR;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease; ss.

XX Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT CDS 185..1138
 FT /*tag= a
 FT /product= "osteoprotegerin binding protein"

PN W09846751-A1.

PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98MO-US07584.
 XX
 PR 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 XX
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ;
 XX
 DR WPI; 1998-594578/50.
 DR P-PSDB; AAM83195.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 PS
 PS Claim 1; Fig 4; 47pp; English.
 XX
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 CC
 XX
 SQ Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
 Query Match 46.4%; Score 121.2; DB 19; Length 2274;
 Best Local Similarity 74.8%; Pred. No. 2.1e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCAATCTGACGCTCAGCTTCACTCACTGTTATTATACCATCATATCCCATGAG 63
 DB 657 GCAAGCTTGAAGCTCAGCTTCTGCTCATCTCATATTAATGCCACCGACATCCCATCTG 716
 QY 64 GCT--CATAAACGAGCTTCTCTTCTTGGAAACATGACCAAGATTGGGAAAGCTCCCA 121
 DB 717 GTTCCCATTAAGTAGTGTGCTTCTTGTGACCATGATGGGGTTGGCCACAGATCTCCA 776
 QY 122 ACATGACTTTGAGCAAGCAAGAACTAAGAGTCA-----AAGCATTTATTACCGGAATG 175
 DB 777 ACATGACTTTTAAAGCAAGAACTAAGTAAATCAAGATGCGCTTTTATTACCTGTATG 836
 QY 176 CCGAGATTGCTCTGCAATGCGGTAACCTCAGCAGGCTTAATCTGCGAGGACTTCAAGC 235
 DB 837 CCACATTTGCTTTCGACATCATGAACCTCAGAGAGCTAGCTACAGATATCTTCAAC 896
 QY 236 TA 237
 DB 897 TA 898
 RESULT 13
 ABK40274
 ID ABK40274 standard; cDNA; 2390 BP.
 XX
 AC ABK40274;

XX
 DT 15-JUL-2002 (first entry)
 XX
 DE CDNA encoding human PRO206 polypeptide.
 XX
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cytostatic; neuroprotective; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200153486-A1.
 PN
 PD 26-JUL-2001.
 PD
 PF 11-FEB-2000; 2000MO-US03565.
 PF
 PR 08-MAR-1999; 99MO-US05028.
 PR 11-MAR-1999; 99US-123972P.
 PR 11-MAY-1999; 99US-133459P.
 PR 02-JUN-1999; 99MO-US12252.
 PR 22-JUN-1999; 99US-140650P.
 PR 22-JUN-1999; 99US-140653P.
 PR 20-JUL-1999; 99US-144758P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 17-AUG-1999; 99US-149395P.
 PR 31-AUG-1999; 99US-151689P.
 PR 01-SEP-1999; 99MO-US20111.
 PR 15-SEP-1999; 99MO-US21090.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 01-DEC-1999; 99MO-US28634.
 PR 05-JAN-2000; 2000MO-US00219.
 XX
 PA (GENTECH) GENENTECH INC.
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
 PI Masters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-205567/26.
 DR P-PSDB; AA086148.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for
 PT treating benign or malignant tumours, leukemias and lymphoid
 PT malignancies, inflammatory, angiogenic and immunologic disorders -
 XX
 PS Claim 50; Fig 41; 302pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,
 CC bladder, breast, etc), leukemias and lymphoid malignancies, other
 CC disorders such as neuronal, glial, astrocytic, hypothalamic, glandular,
 CC macrophagal, stromal and blastocoele disorders, inflammatory, immune
 CC and angiogenic disorders. The polynucleotide sequences are also
 CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
 CC polypeptides of the invention.
 XX
 SQ Sequence 2390 BP; 778 A; 417 C; 506 G; 688 T; 1 other;
 Query Match 46.4%; Score 121.2; DB 24; Length 2390;
 Best Local Similarity 74.8%; Pred. No. 2.2e-30;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;
 QY 4 GCAATCTGACGCTCAGCTTCACTCACTGTTATTATTAACCATCATATCCCATGAG 63
 DB 778 GCAAGCTTGAAGCTCAGCTTCTGCTCATCTCATATTAATGCCACCGACATCCCATCTG 837
 QY 64 GCT--CATAAACGAGCTTCTTCTTGGAAACATGACCAAGATTGGGAAAGCTCTCCA 121

```

Db      838 GTTCCCAATAAGTAGTGTCTGCTTGGTACATGATCGGGGTTGGCCAAAGATCTCCA 897
Qy      122 ACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGCATTATTATCCGGAATG 175
Db      898 ACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGCATTATTATCCGGAATG 957
Qy      176 CCGACATTTCGCTCTGACATCGCGTAACTCAGACGCGCTAAGCTCTGACGAGACCTTCAGC 235
Db      958 CCAACATTTCGCTCTGACATCATGAAACTTCAGAGACCTAAGCTACAGAGTATCTTCAC 1017
Qy      236 TA 237
Db      1018 TA 1019

RESULT 14
AA80223
ID      AA80223 standard; cDNA; 1823 BP.
XX
AC      AA80223;
XX
DT      17-AUG-1999 (first entry)
DE      Human TRANCE encoding cDNA.
XX
KW      TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
KW      TNF-related activation induced cytokine; immune response; cancer;
KW      autoimmune disease; HIV; hypersensitivity; allergen; ds.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      1..738
FT      /*tag= a
XX
XX      MO9929865-A2.
XX      17-JUN-1999.
XX
XX      14-DEC-1998; 98WO-US26486.
XX
XX      11-DEC-1998; 98US-0989479.
XX      12-DEC-1997; 97US-0989479.
XX      03-MAR-1998; 98US-0034099.
XX
PA      (UYRQ ) UNIV ROCKEFELLER.
XX
PI      Choi Y, Josien R, Steinman R, Won B;
XX
XX      WPI: 1999-385609/32.
XX      P-PSDB: AAY17873.
XX
XX      TNF like proteins for treating autoimmunity and cancer
XX
XX      Claim 1; Fig 1; 164bp; English.
XX
XX      The present sequence encodes human TNF-related activation induced
XX      cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX      variants, fragments, derivatives or analogues may be used as modulators
XX      of immune response in a mammal comprising, antisense sequences to
XX      TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX      Agonists and antagonists of TRANCE, can be used to modulate immune
XX      response by increasing or decreasing the life span of mature dendritic
XX      cells and increasing or decreasing T cell activation. These techniques
XX      are especially useful for treating immune system related conditions such
XX      as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX      The TRANCE polypeptides can be used to increase the viability of
XX      dendritic cells in vivo or in vitro, especially when used in conjunction
XX      with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX      CD40L or TNF-alpha).
XX
SQ      Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

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Query Match      45.2%; Score 118; DB 20; Length 1823;
Best Local Similarity 74.0%; Pred. No. 2.3e-29;
Matches 179; Conservative 0; Mismatches 55; Indels 8; Gaps 2;

Qy      4 GCAATCCGAGCGCTGAGCTTCATCATCTGTTATTATNCCATCATATCCCATGAG 63
Db      257 GCAACCTTGAACTGAGCTTCCTTGGCTCATCTGATTAATGACACCGAATCCCATCTG 316
Qy      64 GCT--CATAAAACGAGCTCTTCTCTTGGAAACATGACCAAGATTGGCAAAAGCTCTCCA 121
Db      317 GTTCCCATAAAGTAGAGTGTCTGCTCTGTTGATCATGATGAGGGGTGGGTAAGATCTCCA 376
Qy      122 ACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGCATTATTATCCGGAATG 175
Db      377 ACATGACTTTCAGCAACGGAAGAACTAAGAGTCA-----AAGCATTATTATCCGGAATG 436
Qy      176 CCGACATTTCGCTCTGACATCGCGTAACTCAGACGCGCTAAGCTCTGACGAGACCTTCAGC 235
Db      437 CCAACATTTCGCTCTGACATCATGAAACTTCAGAGACCTAAGCTACAGAGTATCTTCAC 496
Qy      236 TA 237
Db      497 TA 498

RESULT 15
AAF86481
ID      AAF86481 standard; cDNA; 957 BP.
XX
AC      AAF86481;
XX
DT      29-JUN-2001 (first entry)
DE      Rat osteoclast differentiation factor, ODF, coding sequence.
XX
XX      Rat: osteoclast formation inducer; vaccine; gene therapy;
XX      Osteoclast Differentiation Factor; bone; ss.
XX
OS      Rattus sp.
XX
FH      Key
FT      CDS
FT      1..957
FT      /*tag= a
FT      /product= "Rat ODF"
XX
XX      WO200123549-A1.
XX      05-APR-2001.
XX
XX      29-SEP-2000; 2000WO-AU01202.
XX
XX      29-SEP-1999; 99AU-0003147.
XX
PA      (UYMA-) UNIV WESTERN AUSTRALIA.
XX
PI      Xu J, Zheng M;
XX
XX      WPI: 2001-335526/35.
XX      P-PSDB: AAB82092.
XX
XX      Novel nucleic acid encoding rat osteoclast differentiation factor
XX      useful for modulating activity of a cell, e.g., cell proliferation,
XX      cell differentiation and cell viability.
XX
XX      Claim 1; Fig 1; 81bp; English.
XX
XX      The present sequence is the coding sequence for rat Osteoclast
XX      Differentiation Factor (ODF). ODF is thought to be directly involved in
XX      the differentiation of monocytes/macrophages into osteoclasts.
XX      Osteoclasts promote dissolution of the bone matrix and solubilisation of
XX      bone salts. The present sequence is useful in gene therapy, and as
XX      hybridisation probes or primers. ODF protein is useful for modulating the

```

CC activity of cells, e.g., cell proliferation, cell differentiation and
cell viability, as immunogens to generate anti-rat ODF antibodies, and
as vaccines. Anti-rat ODF antibodies are useful in assay methods for
quantifying ODF polypeptides.

XX
SQ Sequence 957 BP: 230 A; 260 C; 256 G; 211 T; 0 other;

Query Match 39.1%; Score 102; DB 22; Length 957;
Best Local Similarity 69.8%; Pred. No. 4.4e-24;

Matches 169; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

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QY 3 GGCATTCCTGACGCTCAGCCTTCTCACTCATCTTGTATTATACCATCAATATCCCATGA 62
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 GGCACGCTGAGGCTGCGCTTGTCTCACCCTCACCATCAATGCTGCCGACATCCCATCG 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 GG--CTCATTAAGAGAGTCTTTCTTGGAAACATGACCAAGATTGGCAACGCTTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 GGTTCCTAATAAGTCAGTCTGTCTCTTGGTACCATGATGAGGCTGGCCAAAGATCTCT 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 AACATGACTTTCAGCAACGGAATAAGAGTCA-----AAGCATTTATTACCGAAT 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 AACATGACGTTAAGCAACGGAATAAGGTTAACCAAGATGGCTTCTATTACCTGTAC 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 GCGACATTTGCTCTGACATCGGCTAACCTCAGCAGGCTTAAGTCTGACAGACCTTCA 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 GCCAACATTTGCTTCAAGCATCATGAACCTCAGGAGCGTACCTGCCGACTATCTTCAG 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 CT 236
    ||
Db 715 CT 716
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Search completed: December 8, 2002, 17:26:15

Job time : 81.3192 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 16:41:40 ; Search time 558.919 Seconds
(without alignments)
13590.225 Million cell updates/sec

Title: US-09-880-457-1_COPY_486_746
Sequence: 1 atggcaatcctgacgcctcag.....gtaattgagaatcattcac 261

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_sts:*
26: em_un:*
27: em_vl:*
28: em_da:*
29: em_hg:*
30: em_hum:*
31: em_in:*
32: em_mu:*
33: em_om:*
34: em_ov:*
35: em_ph:*
36: em_pl:*
37: em_ro:*
38: em_sts:*
39: em_un:*
40: em_vl:*
41: em_da:*

Result No.	Score	Query Match	Length	DB ID	Description
1	251	96.2	1186	6	AX358828 Sequence
2	251	96.2	1186	6	AX362321 Sequence
3	249.4	95.6	1657	2	AC104794 Homo sapi
4	249.4	95.6	1907	9	AC010969 Homo sapi
5	121.2	46.4	818	9	AB064268 Homo sapi
6	121.2	46.4	911	9	AB061227 Homo sapi
7	121.2	46.4	930	9	AB037599 Homo sapi
8	121.2	46.4	954	6	AR156434 Sequence
9	121.2	46.4	954	6	AR164148 Sequence
10	121.2	46.4	954	6	AX147989 Sequence
11	121.2	46.4	954	6	AX451895 Sequence
12	121.2	46.4	972	9	AB064270 Homo sapi
13	121.2	46.4	1034	9	AB064269 Homo sapi
14	121.2	46.4	1201	9	AF019047 Homo sapi
15	121.2	46.4	2271	6	AF053712 Homo sapi
16	121.2	46.4	2390	6	AX201362 Sequence
17	118	45.2	1823	9	AF013171 Homo sapi
18	102	39.1	957	10	AF187319 Homo sapi
19	97.8	37.5	113451	2	AC023297 Homo sapi
20	97.8	37.5	200724	9	AL139382 Human DNA
21	95.6	36.6	754	10	AB032772 Homo sapi
22	95.6	36.6	864	10	AB032771 Homo sapi
23	95.6	36.6	951	6	E34350 DNA and pro
24	95.6	36.6	951	6	E34350 DNA and pro
25	95.6	36.6	951	10	AB008426 Mus muscu
26	95.6	36.6	951	10	AB036798 Mus muscu
27	95.6	36.6	1630	6	AR156433 Sequence
28	95.6	36.6	1630	6	AR164147 Sequence
29	95.6	36.6	1630	6	AX147987 Sequence
30	95.6	36.6	1694	6	AX451897 Sequence
31	95.6	36.6	2191	6	AR157058 Sequence
32	95.6	36.6	2191	6	AX140162 Sequence
33	95.6	36.6	2225	10	AF019048 Mus muscu
34	95.6	36.6	2237	10	AF013170 Mus muscu
35	95.6	36.6	2295	6	AR062119 Sequence
36	95.6	36.6	2295	10	AF053713 Mus muscu
37	91	34.9	522	6	AX232589 Sequence
38	84.8	32.5	127812	2	AC094149 Ratius no
39	81.6	31.3	2029	6	E34349 DNA and pro
40	81.6	31.3	2029	10	AB022039 Mus muscu
41	81.6	31.3	276831	2	AC126690 Mus muscu
42	37.2	14.2	142588	2	AC113992 Mus muscu
43	36.8	14.1	166759	9	AC023297 Homo sapi
44	36.8	14.1	169960	9	AC007716 Homo sapi
45	36.8	14.1	169960	9	AC006440 Homo sapi

ALIGNMENTS

RESULT 1
AX358828
LOCUS AX358828
DEFINITION Sequence 81 from Patent WO0193983.
ACCESSION AX358828
VERSION AX358828.1 GI:18675315
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: WO 0193983-A 81 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES Location/Qualifiers
 source 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 96.2%; Score 251; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. NO. 2.4e-68;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTATTATATACCATCATATCCCAT 60
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 Db 447 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTATTATATACCATCATATCCCAT 506
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QY 61 GAGGCTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 120
 |||||||
 Db 507 GAGGCTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 566
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QY 121 AACATGACTTCAGCAAGCAAACTAGAGTCAAGGCATTATTACCGGAATGCCGAC 180
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 Db 567 AACATGACTTCAGCAAGCAAACTAGAGTCAAGGCATTATTACCGGAATGCCGAC 626
 |||||||

QY 181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGACCTTCAGTATG 240
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 Db 627 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGACCTTCAGTATG 686
 |||||||

QY 241 TGTAAATTGAG 251
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 Db 687 TGTAAATTGAG 697
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RESULT 2
 AX362321 1186 bp DNA linear PAT 15-FEB-2002
 LOCUS Sequence 81 from Patent WO0208288.
 ACCESSION AX362321
 VERSION AX362321.1 GI:18694618
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 Baker, R.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 81 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..1186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 314 a 285 c 299 g 288 t
 ORIGIN

Query Match 96.2%; Score 251; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. NO. 2.4e-68;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTATTATATACCATCATATCCCAT 60
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 Db 447 ATGGCAATCTGAGCGCTCAGCCTTCACATCATCTGTATTATATACCATCATATCCCAT 506
 |||||||

QY 61 GAGGCTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 120
 |||||||
 Db 507 GAGGCTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGCTTCC 566
 |||||||

QY 121 AACATGACTTCAGCAAGCAAACTAGAGTCAAGGCATTATTACCGGAATGCCGAC 180
 |||||||
 Db 567 AACATGACTTCAGCAAGCAAACTAGAGTCAAGGCATTATTACCGGAATGCCGAC 626
 |||||||

QY 181 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGACCTTCAGTATG 240
 |||||||
 Db 627 ATTTGCTCTCGACATCGCGTAACCTCAGCAGCGCTTAACCTGCGAGACCTTCAGTATG 686
 |||||||

QY 241 TGTAAATTGAG 251
 |||||||
 Db 687 TGTAAATTGAG 697
 |||||||

RESULT 3
 AC104794 165707 bp DNA linear HTG 30-APR-2002
 LOCUS Homo sapiens chromosome 2 clone RP11-254F7, WORKING DRAFT SEQUENCE,
 3 unordered pieces.
 AC104794
 AC104794.3 GI:20340520
 VERSION HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 KEYWORDS Homo sapiens.
 SOURCE
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 1 (bases 1 to 165707)
 WATERSTON, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 165707)
 REFERENCE
 2 (bases 1 to 165707)
 WATERSTON, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2001) Genome Sequencing Center, Washington
 MO 63108, USA
 3 (bases 1 to 165707)
 WATERSTON, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2002) Genome Sequencing Center, Washington
 MO 63108, USA
 COMMENT On Apr 30, 2002 this sequence version replaced gi:1939129.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc/index.shtml>
 Contact: submissions@wustl.edu
 Project Information
 Center project name: H_NH0254F07

 Summary Statistics
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 162662 bases at least Q40
 Consensus quality: 163189 bases at least Q30
 Consensus quality: 164786 bases at least Q20
 Insert size: 167795; agarose-fp
 Quality coverage: 12.78 in Q20 bases; agarose-fp
 Quality coverage: 10.53 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will


```

* be preserved.
* 1 1112: contig of 1112 bp in length
* 1113 1212: gap of unknown length
* 1213 76227: contig of 75015 bp in length
* 76228 76327: gap of unknown length
* 76328 165707: contig of 89380 bp in length.
* 76328 location/Qualifiers
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="2"
    /clone="RP11-254E7"
  1. 1112
    /note="assembly_name:Contig21"
    /note="assembly_name:Contig68"
    /note="assembly_name:Contig69"
  76328. 165707
    /note="assembly_name:Contig69"

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  1. 1112
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  1213. 76227
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  76328. 165707
    /note="assembly_name:Contig69"

misc_feature
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BASE COUNT
  42887 a 42242 c 39083 g 41295 t 200 others

ORIGIN
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Best Local Similarity 99.6%; Pred. No. 7e-68;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAATCTGACGCTCACTGCTTCTTATATACCAATATCCCAT 60
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DB 41120 ATGGCAATCTGACGCTCACTGCTTCTTATATACCAATATCCCAT 41179
    |||
QY 61 GAGGCTCAATGAGAGTCTTCTTGTGGAACATGACCAAGATTGGCAACGCTCC 120
    |||
DB 41180 GAGGCTCAATGAGAGTCTTCTTGTGGAACATGACCAAGATTGGCAACGCTCC 41239
    |||
QY 121 AACATGACTTTGCAAGCAAGAACTAGAGTCAAGGCAATTTATACCGGATGCCGAC 180
    |||
DB 41240 AACATGACTTTGCAAGCAAGAACTAGAGTCAAGGCAATTTATACCGGATGCCGAC 41299
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QY 181 ATTTGCTCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 240
    |||
DB 41300 ATTTGCTCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGAC 41359
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QY 241 TGTATTTGAG 251
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DB 41360 TGTATTTGAG 41370
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```

```

REFERENCE
AUTHORS
  4 (bases 1 to 190748)
  Waterston,R.H.
TITLE
  Direct Submission
JOURNAL
  Submitted (19-APR-2001) Genome Sequencing Center, Washington
  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
  MO 63108, USA
REFERENCE
AUTHORS
  5 (bases 1 to 190748)
  Waterston,R.H.
TITLE
  Direct Submission
JOURNAL
  Submitted (20-APR-2001) Genome Sequencing Center, Washington
  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
  MO 63108, USA
REFERENCE
AUTHORS
  6 (bases 1 to 190748)
  Waterston,R.
TITLE
  Direct Submission
JOURNAL
  Submitted (07-NOV-2001) Department of Genetics, Washington
  University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
  On Apr 19, 2001 this sequence version replaced gi:11128441.
COMMENT
  -----
  Center: Washington University Genome Sequencing Center
  Center code: WUGSC
  Web site: http://genome.wustl.edu/gsc
  Contact: saplens@wustl.wustl.edu
  -----
  Summary Statistics
  Center project name: H.NH00950D17
  -----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPI1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, R., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://backpac.med.buffalo.edu>)

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPI1-521D12. Actual start of this clone is at base position 1 of RPI1-95D17; actual end is at base position 190748 of RPI1-95D17.

There are polymorphic base differences between RPI1-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish RPI1-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Size information from restriction digest suggests that the full repeat may not be represented.

```

FEATURES
source
  1. 190748
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="2"

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RESULT 4
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LOCUS          Homo sapiens BAC clone RP11-95D17 from 2, complete sequence.
DEFINITION
AC010969
AC010969
AC010969.11 GI:13677120
VERSION
KEYWORDS
SOURCE
  HTG.
  Homo sapiens.
  Homo sapiens.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
  1 (bases 1 to 190748)
  Toward a complete human genome sequence
  Sulston, J.E. and Waterston, R.
  Genome Res. 8 (11), 1097-1108 (1998)
JOURNAL
  99063792
MEDLINE
  9847074
PUBMED
  2 (bases 1 to 190748)
  Sun, H., Abbott, A. and Le, T.P.
  The sequence of Homo sapiens BAC clone RP11-95D17
  Unpublished
  3 (bases 1 to 190748)
  Waterston, R.H.
  Direct Submission
  Submitted (28-SEP-1999) Genome Sequencing Center, Washington
  University School of Medicine, 4444 Forest Park Parkway, St. Louis,
  MO 63108, USA

```

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repeat_region 323..805 /rpt_family="L1"
repeat_region 806..1114 /rpt_family="Alu"
repeat_region 1449..1567 /rpt_family="MIR"
repeat_region 2179..2369 /rpt_family="MIR"
repeat_region 2626..3646 /rpt_family="L2"
repeat_region 3716..3745 /rpt_family="AT_rich"
repeat_region 3798..4101 /rpt_family="Alu"
repeat_region 4196..5255 /rpt_family="L1"
repeat_region 5256..5559 /rpt_family="Alu"
repeat_region 5560..6453 /rpt_family="L1"
repeat_region 6939..6969 /rpt_family="MIR"
repeat_region 7701..8007 /rpt_family="Alu"
repeat_region 8242..8532 /rpt_family="MERL_type"
repeat_region 8533..8834 /rpt_family="Alu"
repeat_region 8835..9300 /rpt_family="MERL_type"
repeat_region 9322..9647 /rpt_family="L2"
repeat_region 9652..9784 /rpt_family="MALR"
repeat_region 9784..9848 /rpt_family="Alu"
repeat_region 9862..10061 /rpt_family="L1"
repeat_region 10062..10360 /rpt_family="Alu"
repeat_region 10361..10646 /rpt_family="L1"
repeat_region 10647..10948 /rpt_family="Alu"
repeat_region 10949..11090 /rpt_family="L1"
repeat_region 11135..11420 /rpt_family="Alu"
repeat_region 11424..11704 /rpt_family="L1"
repeat_region 11705..12015 /rpt_family="Alu"
repeat_region 12016..12045 /rpt_family="L1"
repeat_region 12047..12327 /rpt_family="Alu"
repeat_region 12335..12416 /rpt_family="L1"
repeat_region 12467..12594 /rpt_family="Alu"
repeat_region 12596..12678 /rpt_family="L1"
repeat_region 12698..12954 /rpt_family="Alu"
repeat_region 12955..13065 /rpt_family="L1"
repeat_region 13194..13433 /rpt_family="L2"

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 Best Local Similarity 99.68; Pred. No. 7e-68;
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QY 241 TGTAAATTGAG 251
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Db 174245 TGTAAATTGAG 174235

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RESULT 5
AB064268 818 bp mRNA linear PRI 26-DEC-2001
LOCUS Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor
DEFINITION kappa B ligand 3, complete cds.
ACCESSION AB064268
VERSION AB064268.1 GI:18143616
KEYWORDS Homo sapiens cDNA to mRNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 818)
AUTHORS Ikeda,T. and Kuroyama,H.

```

TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: toru.pch2@med.tmd.ac.jp, Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)

FEATURES

source

Location/Qualifiers
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ORIGIN

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Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACGCTCAGCTTCACTCATCTGTATTAATCATCATATCCCATGAG 63
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QY 64 GCT--CATAAACGAGCTTTCTTCTTGGAAACATGACCAAGATTGGGCAACGCTCCA 121
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DB 457 ACATGACTTTGACGACGAAACCTAAGTAAATCAGATGAGCTTTTATACCTGTATG 516
QY 176 CCGACATTTGCTCTGACATCGCTAAGCTCAGACGCTTAAGCTGACGACCTTCAAG 235
DB 517 CCAACATTTGCTTGGACATCATGAACCTTCAAGACCTAGCTACAGATATCTTCAAC 576
QY 236 TA 237
DB 577 TA 578

RESULT 6
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LOCUS Homo sapiens mRNA for hRANKL 2, complete cds.
DEFINITION AB061227
ACCESSION AB061227.1 GI:16610212
VERSION
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Ikeda, T., Kuroyama, H. and Hirokawa, K.
TITLE Human RANKL Isoform
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 911)
AUTHORS Ikeda, T. and Kuroyama, H.
TITLE Direct Submission
JOURNAL Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical and Dental University, Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.pch2@med.tmd.ac.jp,

Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)

FEATURES

source

CDS

Location/Qualifiers
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BASE COUNT 253 a 211 c 217 g 230 t
ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 911;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCCGACGCTCAGCTTCACTCATCTGTATTAATCAATCATATCCCATGAG 63
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QY 122 ACATGACTTTGACGACGAAACCTAAGAGTCA-----AAGGCATTATTACCGGAATG 175
DB 550 ACATGACTTTGACGACGAAACCTAAGTAAATCAGATGAGCTTTTATACCTGTATG 609
QY 176 CCGACATTTGCTCTGACATCGCTAAGCTCAGACGCTTAAGCTGACGACCTTCAAG 235
DB 610 CCAACATTTGCTTGGACATCATGAACCTTCAAGACCTAGCTACAGATATCTTCAAC 669
QY 236 TA 237
DB 670 TA 671

RESULT 7
AB037599 930 bp mRNA linear PRI 19-MAR-2002
LOCUS Homo sapiens mRNA for SODF/TRANCE, complete cds.
DEFINITION AB037599
ACCESSION AB037599.1 GI:6863047
VERSION
KEYWORDS
SOURCE Homo sapiens male tongue epithelial-like squamous cell carcinoma cell line: SCC-4 cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Nagai, M., Kyakumoto, S. and Sato, N.
TITLE Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation
JOURNAL Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)
MEDLINE 20175237
REFERENCE 2 (bases 1 to 930)
AUTHORS Nagai, M., Kyakumoto, S. and Sato, N.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchamaru, Morioka, Iwate 020-8505, Japan (E-mail: magai@iwate-med.ac.jp, Tel: +81-19-651-5111 (ex. 4436), Fax: +81-19-654-4147)

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Query Match      46.4%; Score 121.2; DB 9; Length 930;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATTCCTGAGCGCTCAGCCTTCACTCACTCTTGTATTATACATCAATATCCATGAG 63
DB 348 GCAAGCTTGAAGCTCAGCGCTTTGCTCATCTCATATTATGCCACCGCATCCATCTG 407
QY 64 GCT--CATAAACGAGCTCTCTCTCTGGAACATGACCAAGATTGGGAACGTCCTCA 121
DB 408 GTTCCCATTAAGTAGTCTGTCTCTTGTGACATGATGGGGGCGGCAAGATCTCCA 467
QY 122 ACATGACTTTCAGCAGGAACTAAGAGTCA-----AAGGCAATTATTACCGGAATG 175
DB 468 ACATGACTTTCAGCAGGAACTAAGAGTCA-----AAGGCAATTATTACCGGAATG 527
QY 176 CCGACATTTGCTCTGACATCGCTTAACCTCAGACGCGCTTAACCTGACAGCCTTCAGC 235
DB 528 CCACATTTGCTTTCGACATCATGAACTTAATACAGAGATGGCTTTATTACCTGTATG 587
QY 236 TA 237
DB 588 TA 589

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RESULT 8
LOCUS      AR156434
DEFINITION Sequence 12 from patent US 6242213.
ACCESSION  AR156434
VERSION     AR156434.1 GI:15125138
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 954)
AUTHORS    Anderson, D.M.
TITLE       Isolated DNA molecules encoding RANK-L
JOURNAL     Patent: US 6242213-A 12 05-JUN-2001;
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Query Match      46.4%; Score 121.2; DB 6; Length 954;
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Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

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DB 593 ACATGACTTTCAGCAGGAACTAAGAGTCA-----AAGGCAATTATTACCGGAATG 652
QY 176 CCGACATTTGCTCTGACATCGCTTAACCTCAGACGCGCTTAACCTGACAGCCTTCAGC 235
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QY 236 TA 237
DB 713 TA 714

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RESULT 9
LOCUS      AR164148
DEFINITION Sequence 12 from patent US 6271349.
ACCESSION  AR164148
VERSION     AR164148.1 GI:16235114
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 954)
AUTHORS    Dougal, W.C. and Galibert, L.
TITLE       Receptor activator of NF- $\kappa$ B.
JOURNAL     Patent: US 6271349-A 12 07-AUG-2001;
FEATURES
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BASE COUNT  255 a      239 c      227 g      233 t
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Query Match      46.4%; Score 121.2; DB 6; Length 954;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

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QY 236 TA 237
DB 713 TA 714

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ACCESSION  AX147989
VERSION     AX147989.1 GI:14346964
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SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 954)
AUTHORS Anderson, D.M. and Hughes, A.E.
TITLE Receptor activator of nf-kappa b
JOURNAL Patent: WO 0136637-A 12 25-MAY-2001;
Immunex Corporation (US)
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BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 46.4%; Score 121.2; DB 6; Length 954;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCGTCAGCGCTCAACCTCATCTGTTATTAATCATCATATCCCATGAG 63
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QY 64 GCT--CATTAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGTCCTCA 121
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QY 236 TA 237
DB 713 TA 714

RESULT 11
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LOCUS
DEFINITION Sequence 5 from Patent WO0224896.
ACCESSION AX451895
VERSION AX451895.1 GI:21698735
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Dougall, W.C.
TITLE Screening assays for agonists or antagonists of receptor activat or
of nf-kb
JOURNAL Patent: WO 0224896-A 5 28-MAR-2002;
IMMUNEX CORPORATION (US)
FEATURES
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BASE COUNT 255 a 239 c 227 g 233 t

ORIGIN

Query Match 46.4%; Score 121.2; DB 6; Length 954;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

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DB 473 GCAAGCTTGAGAGCTCAGCCCTTTGCTCATCTCATATTATGCGCAGCATCCCATCTG 532

QY 64 GCT--CATTAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGGCAACGTCCTCA 121
DB 533 GTTCCCATTAAGTAGTGTGCTGCTCATCTCATATTATGCGGCTTGGGCAAGATCTCCA 592

QY 122 ACATGACTTTCAGCAGCAAACTAAGATCA-----AAGCATTTATTACCGGAATG 175
DB 593 ACATGACTTTCAGCAGCAAACTAAGATCAAGATGAGTGTGCTTATTACCTGTATG 652

QY 176 CCGCATTTGCTCGACATGCGCTTAACCTGACGAGCCTTACGCGAGCCTTCAG 235
DB 653 CCAACATTGCTTTCGACATGAACTTCAGGAGACCTACGATCAGATCTTCAAC 712

QY 236 TA 237
DB 713 TA 714

RESULT 12
AB064270 972 bp mRNA linear PRI 26-DEC-2001
LOCUS
DEFINITION Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
ACCESSION AB064270
VERSION AB064270.1 GI:18143620
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Ikeda, T., Kuroyama, H. and Hirokawa, K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 972)
AUTHORS Ikeda, T. and Kuroyama, H.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Immunology, Graduate
School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail: tohru.ikeda@tmd.ac.jp, Tel: 81-3-5803-5176,
Fax: 81-3-5803-0123)

FEATURES
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BASE COUNT 270 a 219 c 249 g 234 t
ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 972;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

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QY 176 CCGACATTTGCTCTGACATCGCTAAGCTGACGAGGCTTAAGCTGACGAGCTTCAAGC 235
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QY 236 TA 237
DB 731 TA 732

RESULT 13
AB064269 1034 bp mRNA linear PRI 26-DEC-2001
LOCUS
DEFINITION Homo sapiens hRANKL 1 mRNA for receptor activator of nuclear factor
ACCESSION AB064269
VERSION AB064269.1 GI:18143618
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1034)
AUTHORS Ikeda,T. and Kuroyama,H.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Immunology, Graduate
School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail: tohru.phd2med.tmd.ac.jp, Tel:81-3-5803-5176,
Fax:81-3-5803-0123)

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TLESQDTKLIPDSCRRIKAFQAVOKELQHIIVSGHIAERAMVDGSWLDIAKRSKLE
AQPFAH/ITINATDIPSGSHKYSLSWYHDMGMAKISNMTFSGKLIIVNODGFYLYA
EAPFPAHLITINATDIPSGSHKYSLSWYHDMGMAKISNMTFSGKLIIVNODGFYLYA

NICPRHETSGDLATEYLOLVYVYKTSIKIPSSHTLKGSGSTKXWNSERHFYSIN
VGFEFKLRSGSEISIEVSNPSLDPDQATYTGARKVDID"

BASE COUNT 275 a 257 c 265 g 237 t
ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 1034;
Best Local Similarity 74.8%; Pred. No. 2.8e-27;
Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCAATCTGACGCTCAGCCTTCACTCATCTGTTATTAATACATCAATATCCATGAG 63
DB 553 GCAAGCTTGAAGCTCAGCCTTTGCTCATCTCATTAATATGACACGACATCCATCTG 612
QY 64 GCT--CATAAACAGAGCTCTTCTTCTTGGAAACATGACCAAGATTGGGCAAGCTGCCA 121
DB 613 GTTCCCATTAAGTGAAGTGTCTCTCTTGTACCATGATGGGGTGGCCAAAGATCTCCA 672
QY 122 ACATGACTTTGACGAAAGGAAACTAAGATCA-----AAGCATTTATTAACCGGAATG 175
DB 673 ACATGACTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 732
QY 176 CCGACATTTGCTCTGACATCGCTAAGCTGACGAGGCTTAAGCTGACGAGCTTCAAGC 235
DB 733 CCAACATTTGCTTTCGACATCATGAACCTTCAAGAGACCTAGCTACAGATATCTTCAAC 792
QY 236 TA 237
DB 793 TA 794

RESULT 14
AF019047 2201 bp mRNA linear PRI 22-NOV-1997
LOCUS
DEFINITION Homo sapiens receptor activator of nuclear factor kappa B ligand
ACCESSION AF019047
VERSION AF019047.1 GI:2612921
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2201)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
JOURNAL Nature 390 (6656), 175-179 (1997)
MEDLINE 98032977
PUBMED 9367155

REFERENCE 2 (bases 1 to 2201)
AUTHORS Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA

FEATURES
source
1. .2201 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="13q14"
1. .2201
/gene="RANKL"
129. .1082
/note="receptor activator of nuclear factor kappa B
ligand"

gene
CDS
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/protein_id="AAB86811.1"
/db_xref="GI:2612922"

/translation="MRRASHDYTKYLNGSEEMGGPGAPHEGLHAPPPEPHOPPA
 SSMFVALLGLIGVVCVALFEYFPAQMDPNRISDGTGHCYIRILRLHENDFODT
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 EAOPEAHILINATDIPSGSHKYSLSGMYHIDRGMAKISNMFTSNGKLIVNDGFYLLA
 NICFRHETSGDLATFYLDMYVYTKISIKIPSSHLIMKGGSTKYWSGNSSEHFYSIN
 VGGFRLRSGEELISVSNPSLDPDODATYFCAFVRDID"

BASE COUNT 658 a 429 c 497 g 617 t
 ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 2201;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCTGAGGCTCAACCTGATGTTATTAATACATCAATATCCATGAG 63
 DB 601 GCAAGCTTGAAGCTCAACCTTTGCTCATCTCACTATTAAAGCCAGCATCCCATCTG 660
 QY 64 GCT--CATAAAGAGCTCTTCTCTTGGAAACATGACCAAGATTGGCCAAAGCTCTCA 121
 DB 661 GTTCCCATTAAGTAGTCTGCTCTGTGATCATGATGCGGGGTTGGGCCAAGATCTCA 720
 QY 122 ACATGACTTTCAGCAGGAAACTAAGAGTCA-----AAGCATTTATTACCGGAATG 175
 DB 721 ACATGACTTTAGCAATGAAACTAATAGTTATCAGAGATGGCTTTTATTAATCTGTATG 780
 QY 176 CCGACATTTGCTCTCGACATCGCTTAACCTCAGAGGCTTCACTGAGGACCTTCAGC 235
 DB 781 CCAACATTTGCTTTCGACATCATGAACTTCAGGAGACCTTCACTACAGAGTATCTTCAAC 840
 QY 236 TA 237
 DB 841 TA 842

RESULT 15
 AF053712 2271 bp mRNA linear PRI 09-MAY-1998
 LOCUS AF053712 Homo sapiens osteoprotegerin ligand mRNA, complete cds.
 DEFINITION AF053712
 ACCESSION AF053712
 VERSION AF053712.1 GI:3057145
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 2271)
 Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
 Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
 Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Caparrelli, C., Eli, A.,
 Olan, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
 Delaney, J. and Boyle, W.J.

Osteoprotegerin ligand is a cytokine that regulates osteoclast
 differentiation and activation
 Cell 93 (2), 165-176 (1998)

JOURNAL MEDLINE 98227661
 PUBMED 9568710
 REFERENCE 2 (bases 1 to 2271)
 Boyle, W.J.
 Direct Submission
 Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
 One Amgen Center Drive, Thousand Oaks, California 91320, USA
 TITLE JOURNAL
 FEATURES
 SOURCE

CDS

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 /db_xref="taxon:9606"
 185..1138
 /function="regulates osteoclast differentiation and
 activation"
 /codon_start=1
 /product="osteoprotegerin ligand"
 /protein_id="AAC39731.1"
 /db_xref="GI:3057146"
 /translation="MRRASHDYTKYLNGSEEMGGPGAPHEGLHAPPPEPHOPPA"

SRSMFVALLGLIGVVCVALFEYFPAQMDPNRISDGTGHCYIRILRLHENDFODT
 TLESODTKLIPSCRIKOFQAVOKELOHIVGSOHIREKAMVDGSLDLAKRSKL
 EAOPEAHILINATDIPSGSHKYSLSGMYHIDRGMAKISNMFTSNGKLIVNDGFYLLA
 NICFRHETSGDLATFYLDMYVYTKISIKIPSSHLIMKGGSTKYWSGNSSEHFYSIN
 VGGFRLRSGEELISVSNPSLDPDODATYFCAFVRDID"

BASE COUNT 658 a 462 c 522 g 629 t
 ORIGIN

Query Match 46.4%; Score 121.2; DB 9; Length 2271;
 Best Local Similarity 74.8%; Pred. No. 2.8e-27;
 Matches 181; Conservative 0; Mismatches 53; Indels 8; Gaps 2;

QY 4 GCATCCTGAGGCTCAACCTGATGTTATTAATACATCAATATCCATGAG 63
 DB 657 GCAAGCTTGAAGCTCAACCTTTGCTCATCTCACTATTAAAGCCAGCATCCCATCTG 716
 QY 64 GCT--CATAAAGAGCTCTTCTCTTGGAAACATGACCAAGATTGGCCAAAGCTCTCA 121
 DB 717 GTTCCCATTAAGTAGTCTGCTCTGTGATCATGATGCGGGGTTGGGCCAAGATCTCA 776
 QY 122 ACATGACTTTCAGCAGGAAACTAAGAGTCA-----AAGCATTTATTACCGGAATG 175
 DB 777 ACATGACTTTAGCAATGAAACTAATAGTTATCAGAGATGGCTTTTATTACCTGTATG 836
 QY 176 CCGACATTTGCTCTCGACATCGCTTAACCTCAGAGGCTTCACTGAGGACCTTCAGC 235
 DB 837 CCAACATTTGCTTTCGACATCATGAACTTCAGGAGACCTTCACTACAGAGTATCTTCAAC 896
 QY 236 TA 237
 DB 897 TA 898

Search completed: December 8, 2002, 18:32:01
 Job time : 678.919 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 17:16:58 ; Search time 2565.48 Seconds
(without alignments)
7329.213 Million cell updates/sec

Title: us-09-880-457-1

Sequence: 1 aaaagaggaataatcaagaa.....taataaaggaggaataatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_yrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95.8	8.3	659	AG107545	AG107545 Pan trogl
2	84.8	7.3	612	BH267783	BH267783 CH230-186
3	75.8	6.5	362	AV653073	AV653073 AV653073
4	48	4.1	598	BF724774	BF724774 bx08e07.y
5	46.4	4.0	487	B92778	B92778 CTT-HSP-216
6	44	3.8	372	AA337226	AA337226 EST42291

7	44	3.8	550	10	AW966229
C	8	43.8	407	17	AO085343
C	9	43.6	855	17	CNS011PE
C	10	43.4	198	17	BG197160
C	11	43.4	438	17	AO669724
C	12	43.2	355	17	AO013160
C	13	42.4	384	13	BG940945
C	14	42.4	626	17	AG154770
C	15	41.8	276	12	BG203357
C	16	41.8	299	12	BG206497
C	17	41.8	892	17	CNS03FPR
C	18	41.8	975	17	CNS02KBD
C	19	41.8	979	17	B18713
C	20	41.6	502	17	AO142682
C	21	41.4	615	17	AO538505
C	22	40.6	444	9	A1223309
C	23	40.6	449	9	A1286243
C	24	40.4	645	17	B19590
C	25	40.2	277	12	BG184205
C	26	40.2	634	17	AO527342
C	27	40	679	17	AG154560
C	28	40	773	17	AO743573
C	29	39.6	414	9	AA814937
C	30	39.6	641	10	BE081027
C	31	39.6	690	17	AO490150
C	32	39.6	997	17	CNS005TE
C	33	39.6	1027	14	B0050697
C	34	39.2	404	10	AW975966
C	35	39.2	412	9	A1201905
C	36	39.2	644	10	AW749542
C	37	39.2	680	14	BQ182337
C	38	39.2	714	17	AG173653
C	39	39.2	733	13	BM666955
C	40	39.2	345	11	BC026895
C	41	39.2	340	11	BC382085
C	42	39	428	10	AW027590
C	43	39	623	17	AO021146
C	44	38.8	269	14	F03748
C	45	38.8	472	17	AO580608

ALIGNMENTS

RESULT 1
LOCUS AG107545 659 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-112G09.F, genomic survey sequence.
ACCESSION AG107545
VERSION AG107545.1 GI:16728063
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 659)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenho-cho, Tsukuba, Ibaraki, Japan, Kanagawa 230-0045, Japan (E-mail:chimpanzee@sc.riken.go.jp, URL:http://hsp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Rnd process and may have higher chance of clone tracking errors.

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Class: BAC ends.
Location/Qualifiers
1. 612
/organism="Rattus norvegicus"
/strain="BN/SMNSd/MCW"
/db_xref="taxon:10116"
/clone_1lb="CH230-186C1"
/clone_1lb="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SMNSd/MCW) BAC library produced by
Pietet de Jong"

BASE COUNT      168 a      145 c      133 g      166 t

ORIGIN

Query Match      7.3%: Score 84.8; DB 17; Length 612;
Best local Similarity 69.5%; Pred. No. 2.4e-13;
Matches 132; Conservative 0; Mismatches 52; Indels 6; Gaps 1

QY      538  TATCCATGAGGCTCATAAACGACGCTTCTTCTTGGAACATGACCAAGATTGGCAA 597
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      603  TCTCTTAGGTTCCCATTAAGTCAGTCTGCTCTTGATACCATGATCGAGGTGGCCA 544
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      598  AGCTGCGCAACAGACTTTCAGACGAGAACTAGACTCA-----AAGCATTTATT 651
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      543  AGATCTCTTACATGACGTTAGCGAAGAACTAAGGGTTAACCAAGATGGCTTCTATT 484
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      652  ACCGGAATCGACATTTTCTCTCGACATCGGGTACCTCAGACGAGCTTAACCTGCAGG 711
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      483  ACCTGACGCCCAACATTTTCTTCAGGCATCATGAAACCTCAGGAGACTCTGCGGACT 424
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      712  ACCTTCAGCT 721
          | | | | | | | |
DB      423  ATCTTCAGCT 414

RESULT 3
LOCUS      AV653073                      362 bp      mRNA      linear      EST 15-JAN-2002
DEFINITION AV653073 GLC Homo sapiens cDNA clone G1CDB01 3', mRNA sequence.
VERSION    AV653073
ACCESSION  AV653073.1 GI:9874087
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 362)
AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Yu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
            Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
            Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
Source
1..362
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="G1CDB01"
/clone_1lb="GLC"

```

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/dev stage="Adult"
/lab host="SOLR"
/Note="Vector: Bluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      102 a      80 c      78 g      100 t      2 others
ORIGIN
Query Match      6.5%; Score 75.8; DB 10; Length 362;
Best Local Similarity 71.5%; Pred. No. 8.2e-11;
Matches 113; Conservative 0; Mismatches 43; Indels 2; Gaps 1;

QY 465 CAGAGAGATTTGCTAAGATGCAATCCCTGACGCTCAACCTCATCTTGTTA 524
      || || || || || || || || || || || || || || || || || ||
DB 204 CAGGTGTAAGTCTGCGCAAGAGGAGCAAGCTGAGCTGAGCTTGTCTATCTCACTA 263
      || || || || || || || || || || || || || || || || || ||
QY 525 TTAATACCATCATATTCCTCATGAGCTT-CATAAAGCAGCTTCTTCTTGGAACATG 582
      || || || || || || || || || || || || || || || || || ||
DB 264 TTAATGCCACCGACATCCATCTGTTCCCATTAAGTAGCTGCTCTTGTGACATG 323
      || || || || || || || || || || || || || || || || || ||
QY 583 ACCAAGATGGGCAAGCTCTCCCAACATGACTTCAGC 620
      || || || || || || || || || || || || || || || || || ||
DB 324 ATCGGCTGTGGGCCAAGATCTCAACATGACTTTTACG 361
      || || || || || || || || || || || || || || || || || ||

RESULT 4
BF724774/c 598 bp mRNA linear EST 05-JAN-2001
LOCUS      bx08e07.y1 Human Iris cDNA (un-normalized, unamplified): BX Homo
DEFINITION sapiens cDNA clone bx08e07 5', mRNA sequence.
ACCESSION  BF724774
VERSION     BF724774.1 GI:12040685
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 598)
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES      Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
JOURNAL     NEIBANK: EST analysis and bioinformatics for ocular genomics
COMMENT     Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: giraemehelix.nih.gov
            Plate: 08 row: e column: 07
            Seq primer: M13Rpl reverse primer (ABI).
FEATURES
SOURCE      Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="bx08e07"
            /clone_1lb="Human Iris cDNA (un-normalized, unamplified):
            BX"
            /tissue_type="Iris"
            /dev stage="Adult"
            /lab host="EMDH10B"
            /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
            tissue was pooled from 10 individuals ranging in age from
            4-80 years and RNA was extracted. From this pooled sample
            an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
            directionally cloned cDNA library in the pCMVSPORT6 vector
            was constructed at Life Technologies, essentially
            following the protocols of the Superscript Plasmid System
            full details of which are contained in the manufacturer's
            instruction manual (http://www.lifetech.com/). First
            strand synthesis was carried out using a Not I
            primer-adaptor [5'-pGACTAGTCTAGATCGCGACGCGCC(7)15-3'
            ]. Not I blunt end inserts were cloned into the Not I/EcoR
            V sites in the vector. EST analysis was performed on the
            unamplified library at the NIH Intramural Sequencing

```

```

Center (NISC)."
BASE COUNT      161 a      142 c      146 g      149 t
ORIGIN
Query Match      4.1%; Score 48; DB 12; Length 598;
Best Local Similarity 68.8%; Pred. No. 0.011;
Matches 66; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 348 AGTATCTACAGGACGACGATTTTGTGACATTTGGGATTTGTACCAACAAGTCAG 407
      || || || || || || || || || || || || || || || || || ||
DB 96 AGTGTCTCTCTGTGACAGGATGTTCTACGCGGTGGGATATGACATTAACAAGCAG 37
      || || || || || || || || || || || || || || || || || ||
QY 408 ACAAAAACCTTGCTCTGTTGGAGGAGCAATCTAG 443
      || || || || || || || || || || || || || || || || || ||
DB 36 GCAAAAATCCCTGACCTCATGGAACCTGACTTACG 1
      || || || || || || || || || || || || || || || || || ||

RESULT 5
B92778      487 bp DNA linear GSS 25-JUN-1998
LOCUS      CIT-HSP-2164D13.TR CIT-HSP Homo sapiens genomic clone 2164D13, DNA
DEFINITION sequence.
ACCESSION  B92778
VERSION     B92778.1 GI:2975115
KEYWORDS   GSS.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 487)
AUTHORS    Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLES      Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
JOURNAL     Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
COMMENT     Simon,M. and Venter,J.C.
            Use of a random BAC End Sequence Database for Sequence-Ready Map
            Building (1998)
            Unpublished (1998)
            Other_GSSs: CIT-HSP-2164D13.TF
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (Info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES
SOURCE      Location/Qualifiers
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            /db_xref="GDB:7100687"
            /db_xref="taxon:9606"
            /clone="2164D13"
            /clone_1lb="CIT-HSP"
            /sex="Male"
            /cell_type="Sperm"
            /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
            HindIII"
BASE COUNT      147 a      104 c      83 g      152 t      1 others
ORIGIN
Query Match      4.0%; Score 46.4; DB 17; Length 487;
Best Local Similarity 60.2%; Pred. No. 0.03;
Matches 77; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 349 GTATCTACAGGACGACGATTTTGTGACATTTGGGATTTGTGCAACAAGTCAGA 408
      || || || || || || || || || || || || || || || || || ||
DB 182 GTGCCACCTATGTGACACGCAAGTATATGATTTAGAAATTCAGCAAGCAAGACAGA 123
      || || || || || || || || || || || || || || || || || ||
QY 409 CAAAAAACCTTGCTGTGGTGGAGGAGCAATTTAGCAAAAGGAGCAATAGCAAGCAGG 468
      || || || || || || || || || || || || || || || || || ||

```

DB	122	CAAAACACCCTGGCCGTCGACCTTCTATCATTCAGCACTCCAGGACAGAAAGAAAGA	63
QY	469	AGAGAGT 476	
Db	62	TGATATT 55	
RESULT 6			
LOCUS	AA337226		
DEFINITION	EST42291	Endometrial tumor Homo sapiens	CDNA 5' end, mRNA sequence.
ACCESSION	AA337226		
VERSION	AA337226.1	GI:1989784	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fudner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weissbrock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Whi,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodex,A., Kelley,J.C., Liu,L.-I., Mammos,S.H., Hinkle,P.S., Jr., Kelley,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He-M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL	Nature	377 (6547 suppl.)	3-174 (1995)
MEDLINE	96026280		
COMMENT	Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlavage@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi.html) Seq primer: M13 Reverse. Location/Qualifiers 1..372 /organism="Homo sapiens" /db_xref="ARCC (inhost:139297)" /db_xref="taxon:9606" /clone_lib="Endometrial tumor" /sex="female" /dev_stage="adult" /note="Organ: endometrium; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"		
FEATURES			
SOURCE			
BASE COUNT	106 a	78 c	104 g 83 t 1 others
ORIGIN			
Query Match	3.8%	Score 44;	DB 9; Length 372;
Best Local Similarity	70.2%	Pred. No. 0.13;	
Matches	59;	Conservative 0;	Mismatches 25; Indels 0; Gaps 0;
OY	368	CATTTTGGACATTGGGATTTGTACGCAACAGTCAAGCAAAAAACCTGCTGTGT 427	
Db	90	CTGTCTAGACACTTGGGATTCACCAAGTATACGACAAAGACAAAAATCCCTGCTGGA 149	
OY	428	GGAAGACATTTAGCAAGGAA 451	

Db	150	GCAGCTTACATCTTACGATGGCAA	173
RESULT 7			
LOCUS	AW966229	550 bp	mRNA
DEFINITION	EST378302	MAGE resequences, MAGI	Homo sapiens cDNA, mRNA sequence.
ACCESSION	AW966229		
VERSION	AW966229.1	GI:8156065	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Hagde,P., Qi,R., Abernathy,K., Dharrap,S., Gaspar,R., Gay,C., Holt ,J.E., Speed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.		
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 224 Seq primer: Reverse.		
FEATURES	Location/Qualifiers		
source	1..350 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE resequences, MAGI" /note="Vector: pBluescriptsm"		
BASE COUNT	165 a 107 c 146 g 132 t		
ORIGIN			
Query Match	3.8%;	Score 44;	DB 10;
Best Local Similarity	70.2%;	Pred. No. 0.15;	
Matches	59;	Conservative 0;	Mismatches 25;
		Indels 0;	Gaps 0;
QY	368	CATTTTGTGACGATTGGGATTTGTACGCAACAAGTCAGACAAAACCTGCTCTGCT	427
Db	89	CTTGCTCTAGCACTTGGGATTCACCACTATACATGAGACAAAATCCCTGCGCTGA	148
QY	428	GGAGGCAACATTCAGCAAGGAA	451
Db	149	GCAGCTTACATCTTACGATGGCAA	172
RESULT 8			
LOCUS	AQ085343	407 bp	DNA
DEFINITION	HS.2164.B1.B07.MR.C1T	Approved Human Genomic Sperm Library D	Homo
ACCESSION	AQ085343	sapiens genomic clone plate-2164	Col-13 Row-D, DNA sequence.
VERSION	AQ085343.1	GI:3454560	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (17),	9739-9744 (1999)
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L		

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Sequence Tagged Connector
Plate: 2164 row: D column: 13
Class: BAC ends
High quality sequence stop: 407.

FEATURES

source

Location/Qualifiers

1..407
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2164 Col=13 Row=D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT

120 a 82 c 75 g 129 t 1 others

ORIGIN

Query Match 3.8%; Score 43.8; DB 17; Length 407;
Best Local Similarity 60.5%; Pred. No. 0.16; Mismatches 0; Gaps 0;
Matches 72; Conservative 0; Indels 47; Indels 0;

QY 349 GTATCTACAGGACACGATTTTGTGACATTTGTCAGCAACAGTCAGA 408

Db 126 GTGCCACTATGACACGACGATATGATTCAGATTGACAGCAACAGACAGA 67

QY 409 CAAAAAAGCTTCTGTGTGGAGGACATTCAGCAAGGCAATTCAGCAAG 467

Db 66 CAAAAACACCTCCCTGCTCAAGCTTATCATTCACCTCCAGGAGCAGAAAGAAG 8

RESULT 9

CNSOL1PE

LOCUS

DEFINITION 855 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN06M20 of DrosBAC library from Drosophila melanogaster (fruit
fly) genomic survey sequence.

ACCESSION AL100556

VERSION AL100556.1 GI:5612167

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 855)

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EGRP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (DrosBAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelBAC11.

FEATURES

source

Location/Qualifiers

1..855
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN06M20"
/clone_lib="DrosBAC"
/plasmid="pBelBAC11"
/note="end : SP6"

BASE COUNT

96 a 63 c 75 g 160 t 461 others

ORIGIN

Query Match 3.8%; Score 43.6; DB 17; Length 855;
Best Local Similarity 11.5%; Pred. No. 0.23;
Matches 64; Conservative 148; Mismatches 346; Indels 0; Gaps 0;

QY 393 CAGCAACAAGTCAGACAAAAACCTTCTGCTGGTGAAGGACATTTAGCAAGAG 452

Db 250 MAMMMAMMMACACAAACAMMMAMMMVMMVMMNNNNNNNNNNNNNNNNNNNNNN 309

QY 453 GCAATGACAGGAGGAGGATTTGCTAGAAATGGAATCCGACGTCAGCCTTCAA 512

Db 310 NNNMAMMTTMMAMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 369

QY 513 CTGATCTTTGTTAATATACATCAATATCCATGAGGCTCAAAACGAGCTTTCTCT 572

Db 370 MTMTNTNTNTMTCTTCCMMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 429

QY 573 TCGAATCATGACCAAGATTTGGGCAACGCTTCCAAATGATTCAGCAAGGAAACTA 632

Db 430 NNN 489

QY 633 AGAGTCAAGGACATTTATCCGGAATGCCGACATTTGCTCGACATCGGTACCTCA 692

Db 490 MMTNTTMMNNNG 549

QY 693 CGAGGCTTAATCTGACGACCTTCAAGTATGTTGTAATTTAGCAATCATTCAGTACA 752

Db 550 GNTTNN 609

QY 753 TCAACTATGTACACGATTTGGTGGTGGCCAGAGATCCAAAGCTTAAGACCAAAACC 812

Db 610 TTTTNN 669

QY 813 TGCCTCCAGGAAGAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 872

Db 670 MNN 729

QY 873 CCGTAGAGGAGGAGGAGTGGTGGTGGCTGAGAGCAACGAGATTAATGGCCCTGGAGGC 932

Db 730 KMSGGMGMMVGGSGVSGGVMGGGKSGMMKKKKGTMGVMGVMGGGGGGBMGM 789

QY 933 CCGGGAAGAGATGAGTTT 950

Db 790 KTGWTMTNGTTT 807

RESULT 10

LOCUS BG197160/c 198 bp mRNA linear EST 21-APR-2001

DEFINITION RST16397 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG197160

VERSION BG197160.1 GI:13718847

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 198)

AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
E., Veloso,N., Kilka,A., Hess,D., Cothren,K., Lo,K., Offenbacher,
J., Danzig,J. and Ducar,M.TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)JOURNAL 21227151
MEDLINE
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com

High quality sequence stop: 148.

FEATURES

SOURCE

Location/Qualifiers
1..198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="H1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT

55 a 56 c 41 g 46 t

ORIGIN

Query Match 3.7%; Score 43.4; DB 12; Length 198;
Best Local Similarity 69.4%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 465 CAGGAGAGTATTGCTAGAGATGCGATCGCTGACCTTCACATCTTGT 524

DB 140 CATGCTTAGATCTGGCGCAGAGAGACGCTTGAAGCTCTTGTCTCATCTACTA 81

QY 525 TTATATACATCATATATCCATGAGG 549

DB 80 TTATATGACGACGACATCCATGCTGG 56

RESULT 11

LOCUS

A0669724 438 bp DNA linear GSS 24-JUN-1999

DEFINITION HS.5381_Al_P01.SP6E.RPCI-11 Human Male BAC Library Homo sapiens

ACCESSION A0669724

VERSION A0669724.1 GI:5202558

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 438)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

REFERENCE

AUTHORS

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 957 row: K column: 1

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 438.

FEATURES

SOURCE

Location/Qualifiers
1..438
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 166 a 87 c 62 g 122 t 1 others

ORIGIN

Query Match 3.7%; Score 43.4; DB 17; Length 438;
Best Local Similarity 69.4%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 363 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGT 422

DB 104 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGT 163

QY 423 CTGTGGAGGGAGACATTTTACGCAA 447

DB 164 TTGTGGAGCTTACATTTCTAAATA 188

RESULT 12

LOCUS

A0013160 355 bp DNA linear GSS 06-JUN-1998

DEFINITION CIT-HSP-2298M3.TF CIT-HSP Homo sapiens genomic clone 2298M3, DNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 355)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mcladams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13-21

Class: BAC ends.

Location/Qualifiers
1..355
/organism="Homo sapiens"
/db_xref="GDB:715385"
/db_xref="taxon:9606"
/clone_lib="2298M3"
/clone_id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 113 a 67 c 83 g 92 t

ORIGIN

Query Match 3.7%; Score 43.2; DB 17; Length 355;

Best Local Similarity 60.0%; Pred. No. 0.22; Indels 0; Gaps 0;

Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 363 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGT 422

DB 163 CCAGCATTTTGTGAGCATTTGGATTTGTCAGCAACAGTCAGCAAAAAACCTTGT 222

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:56:14 ; Search time 330.592 Seconds
(Without alignments)
7908.746 Million cell updates/sec

Title: US-09-880-457-1
Perfect score: 1161
Sequence: 1 aaaagagataatcaagaa.....taataaagagagaatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: N_Geneseq-101002.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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25: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	23.1	1186	24	ABK33576
2	126.2	10.9	741	19	AAV69899
3	126	10.9	954	19	AAV69887
4	126	10.9	954	19	AAV41378
5	126	10.9	954	19	AAV41372
6	126	10.9	954	22	AAD15311
7	126	10.9	954	22	AAD08715
8	126	10.9	954	22	AAD05904
9	126	10.9	1945	24	ABK12877

10	126	10.9	2226	24	ABK12876	CDNA encoding huma
11	126	10.9	2271	21	AAZ99964	DNA encoding a hum
12	126	10.9	2274	19	AAV70285	Human osteoprotege
13	126	10.9	2390	24	ABK40274	CDNA encoding huma
14	122.8	10.6	1823	20	AAH80223	Human TRANCE encod
15	102	8.8	957	22	AAH66481	Rat osteoclast dif
16	97	8.4	735	19	AAV69898	Nucleotide acid encod
17	97	8.4	951	19	AAV69900	Nucleotide acid encod
18	97	8.4	951	21	AAH39156	Mouse OBM nucleoti
19	97	8.4	951	21	AAZ99965	DNA encoding a mur
20	97	8.4	951	21	AAZ49024	Osteoclast formati
21	97	8.4	1538	19	AAV69886	Nucleic acid encod
22	97	8.4	1574	22	AAH55526	Nucleotide sequenc
23	97	8.4	1630	19	AAV41377	NF-kB receptor act
24	97	8.4	1630	19	AAV41371	NF-kB receptor act
25	97	8.4	1630	22	AAD15310	Murine receptor ac
26	97	8.4	1630	22	AAD08714	Murine receptor ac
27	97	8.4	1630	22	AAD05903	Murine RANKL (reco
28	97	8.4	2191	19	AAV41489	Murine TRANCE enco
29	97	8.4	2237	20	AAH80224	CDNA encoding mous
30	97	8.4	2237	24	ABK12880	Human osteoprotege
31	97	8.4	2295	19	AAV70284	DNA encoding a mur
32	97	8.4	2299	21	AAZ99966	DNA encoding a mur
33	94.4	8.1	522	22	AAH33365	Mouse CDNA encodin
34	81.6	7.0	2029	21	AAH39155	DNA encoding a syn
35	74.2	6.4	519	21	AAZ99968	DNA encoding a syn
36	74.2	6.4	519	21	AAZ99969	DNA encoding a mur
37	74.2	6.4	519	21	AAZ99972	DNA encoding osteo
38	74.2	6.4	564	21	AAZ99967	DNA encoding a syn
39	74	6.4	564	21	AAZ99970	DNA encoding osteo
40	73.8	6.4	546	21	AAZ99971	DNA encoding osteo
41	63.2	5.4	519	21	AAZ99973	DNA encoding osteo
42	46.2	4.0	1001	21	AAH51592	Human GCLL related
43	44	3.8	659	22	AAH00215	Human reproductive
44	44	3.8	963	22	AAH34950	Human colon cancer
45	44	3.8				

ALIGNMENTS

```
RESULT 1
ABK33576
ID ABK33576 standard; cDNA: 1186 BP.
XX
AC ABK33576;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 81.
XX
DE
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220644P.
PR 25-JUL-2000; 2000US-220665P.
PR 25-JUL-2000; 2000US-220893P.
```

28-JUL-2000; 2000MO-US20710.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001MO-US17092.

(GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 DR P-PSDB; AAU83632.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a colon related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -

XX Claim 2; Figure 81; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK3536-ABK3567 represent human
 CC PRO protein coding sequences of the invention.

XX Sequence 1186 BP; 314 A; 285 C; 299 G; 288 T; 0 other;

XX Query Match 23.1%; Score 268; DB 24; Length 1186;
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-76;
 XX Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 AGAGTATTTGCTAGAAATGCAATCCTGACCTGACCTCAACTCATTCTTTATTAA 528
 DB 430 AGAGTATTTGCTAGAAATGCAATCCTGACCTGACCTCAACTCATTCTTTATTAA 489
 QY 529 TACATCATATATCCATGAGGCTCAATAAAGAGTCTTCTTCTTGGAAACATGACCAAG 588
 DB 490 TACATCATATATCCATGAGGCTCAATAAAGAGTCTTCTTCTTGGAAACATGACCAAG 549
 QY 589 ATTGGGCAAAAGTCTCCCAATGATCTTACGACGAAAGAACTAAGAGTCAAAAGCATTT 648
 DB 550 ATTGGGCAAAAGTCTCCCAATGATCTTACGACGAAAGAACTAAGAGTCAAAAGCATTT 609
 QY 649 ATTACCGGAATGCGCAGATTTTCTCTGCAATCGGTAACCTCAGAGGCGTAACCTGCG 708
 DB 610 ATTACCGGAATGCGCAGATTTTCTCTCTGCAATCGGTAACCTCAGAGGCGTAACCTGCG 669
 QY 709 AGGACCTTACGCTATGCTGTAATTTGAG 736
 DB 670 AGGACCTTACGCTATGCTGTAATTTGAG 697

RESULT 2

AAV69899
 ID AAV69899 standard; cDNA to mRNA; 741 BP.

XX AAV69899;

XX 10-FEB-1999 (first entry)

XX Nucleic acid encoding a human OCIF-binding molecule (OBM).

XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT 1..741
 FT CDS /*tag= a

XX WO9846644-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-JP01728.

XX 02-DEC-1997; 97JP-0332241.

XX 15-APR-1997; 97JP-0097808.

XX 09-JUN-1997; 97JP-0151434.

XX 12-AUG-1997; 97JP-0217897.

XX 21-AUG-1997; 97JP-0224803.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX WPI: 1998-594563/50.

XX P-PSDB; AAM83020.

XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PT Example 28; Pages 121-122; 151pp; Japanese.

XX The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a soluble form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.

XX Sequence 741 BP; 230 A; 153 C; 158 G; 200 T; 0 other;

XX Query Match 10.9%; Score 126.2; DB 19; Length 741;
 XX Best Local Similarity 68.2%; Pred. No. 3.8e-30;
 XX Matches 223; Conservative 0; Mismatches 93; Indels 11; Gaps 3;

QY 407 GACAAAGAACTGCTGCTGGTGGAGGAGCAATTTAGCAAGGAAGCAATGACAG-- 464
 DB 175 GAATTTACACATATCTGTTGGATCACAGCACATACAGAGCAAGAGCAATGATGATGCGC 234
 QY 465 -CAGAGAGAGTATTTGCTAGAAATGCAATCCTGACGCTCAACTCATCTCTGTT 523
 DB 465 -CAGAGAGAGTATTTGCTAGAAATGCAATCCTGACGCTCAACTCATCTCTGTT 523

Db 235 TCATGTTAGATCTGGCCAGAGGACGAGCTTGAGCTTTTGTCTCATCTCACT 294
 Qy 524 ATTAATACATCATATATCCCATGAGCT--CATAAACGAGCTTTCTTCTTGAAACAT 581
 Db 295 ATTAATGCCACCAACATCCATCTGCTCCATTAAGTGAAGTCTGCTCTTGAGACAT 354
 Qy 582 GACCAAGATTGGGCAACGCTCTCCACATGACTTTCAGCAACGGAACCTAAGAGTCA-- 639
 Db 355 GATCGGGGTTGGGCCAAGATCTCCACATGACTTTAGCAATGGAACCTATAGTTAT 414
 Qy 640 ---AAGCATTTATTAACCGAATGCGACATTTGCTCTGCACATCGGTAACCTCAGCA 695
 Db 415 CAGATGGCTTTTATATACCTGATGCGACATTTGCTTGCACATGAAACCTCAGGA 474
 Qy 696 GGCCTAATCTGCAGGACCTTCAGCTA 722
 Db 475 GACCTAGCTACAGAGATCTTCACTA 501
 RESULT 3
 ID AAV69887 standard; cDNA to mRNA; 954 BP.
 AC AAV69887;
 XX
 DT 10-FEB-1999 (first entry)
 DE Nucleic acid encoding a human OCIF-binding molecule (OBM).
 XX
 DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KM human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /tag= a
 XX
 PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-Jp01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Mashida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 DR WPI; 1998-594563/50.
 DR P-PSDB; AAW83018.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PS
 PS Claim 38; Page 115; 151pp; Japanese.
 CC The present sequence encodes an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence

CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 SQ Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
 Query Match 10.9%; Score 126; DB 19; Length 954;
 Best Local Similarity 72.6%; Pred. No. 5; Le-30;
 Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;
 Qy 465 CAGGAGAGTATTTGCTTAAGATGAGCAATGCTGACGCTTCAACTCATCTTGTGA 524
 Db 449 CATGCTTAGATCTGGCCAAAGAGGACAGCTGAGCTGAGCTTCTTGTCTATCTCACTA 508
 Qy 525 TTATATACATCAATATCCCATGAGGCT--CATAAACGAGCTTTCTTCTTGAAACATG 582
 Db 509 TTATATGACACGACATCCCATCTGCTCCATAAAGTAGTCTGCTCTTGTAACATG 568
 Qy 583 ACCAAGATTGGCAACAGCTCTCCACATGACTTTCAGCAGCAAGGAAACCTAAGAGTCA--- 639
 Db 569 ATCGGGGTTGGGCCAAGATCTCCACATGACTTTTACCAAGGAAACCTAATAGTTATC 628
 Qy 640 ---AAGCATTTTATTAACCGAATGCGACATTTGCTCTGCACATCGGTAACCTCAGCAG 696
 Db 629 AGGATGGCTTTTATTAACCTGATGCGACATTTGCTTGCACATGAAACCTCAGGAG 688
 Qy 697 GCCTAATCTGCAGGACCTTCAGCTA 722
 Db 689 ACCTAGCTACAGAGTATCTCACTA 714
 RESULT 4
 ID AAV41378 standard; cDNA; 954 BP.
 AC AAV41378;
 XX
 DT 08-OCT-1998 (first entry)
 DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 XX
 DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 XX
 KM RANK: necrosis factor-kappa B; NF-kB: receptor activator; human;
 KM immune response; inflammatory response; toxic shock; sepsis;
 KM RANKL: RANK ligand; tumour necrosis factor; TNF; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..954
 FT /tag= a
 FT /product= "human RANKL (ligand for RANK)"
 XX
 PN WO9828426-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US23775.
 XX
 PR 14-OCT-1997; 97US-0064571.
 PR 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0813509.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 PI
 DR WPI; 1998-377657/32.
 DR P-PSDB; AAW69957.
 XX

XX 15-NOV-2001 (first entry)

DE Human receptor activator of NF kappaB ligand (RANKL) cDNA.

XX Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF;

KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;

KW immune response; inflammatory response; graft-versus-host reaction;

KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;

KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT 1.954

FT CDS /tag= a

FT /product= "Human RANK ligand (RANKL) protein"

XX US6271349-B1.

PD 07-AUG-2001.

XX 17-DEC-1998; 98US-0215649.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0077181.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0772330.

PR 07-MAR-1997; 97US-0813509.

PR 22-DEC-1997; 97US-0996139.

XX (IMNV) IMMUNEX CORP.

PA Dougall WC, Galibert L;

XX WPI: 2001-520313/57.

DR P-PSDB; AAE08738.

XX New receptor activator of NF-kappaB (RANK) polypeptides, useful for

PT regulating immune response, in screening for RANK inhibitors, or as an

PT adjunct therapy for disease characterized by neoplastic cells that

PT express RANK

PT Example 7; Column 69-71; 47pp; English.

XX The patent discloses novel receptor activator of nuclear factor (NF)-

CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member

CC of the tumour necrosis factor (TNF) receptor superfamily and associates

CC with TNF receptor associated factor (TRAF) 2 and 3 which are important

CC in the regulation of immune and inflammatory response. The receptors

CC are useful for regulating immune response and in screening for inhibitors

CC of these receptors. The cytoplasmic domain of RANK is used in developing

CC assays for inhibitors of signal transduction, e.g. for screening the

CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,

CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists

CC are useful in ameliorating the negative effects of an inflammatory

CC response that result from triggering of RANK, e.g. in treating toxic

CC shock or sepsis, graft-versus-host reactions, acute inflammatory

CC reactions and the effects of bone resorption. RANK acts as an anti-

CC apoptotic signal and rescue the cells that express RANK from apoptosis.

CC Soluble forms of the receptor are used in vivo or in vitro based

CC screening tests for agonists or antagonists of RANK activity, as

CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit

CC transduction of a signal via RANK. RANK compositions are used in the

CC development of both agonistic and antagonistic antibodies, or as an

CC adjunct therapy for disease characterised by neoplastic cells that

CC express RANK. Compounds that interfere with RANK/TRAF6 interactions

CC are useful for modulating osteoclast function and activities. They

CC are used as inhibitors of diseases associated with excess bone resorption

CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are

CC useful for the expression of recombinant proteins, as probes for analysis

CC of the presence or distribution of RANK transcripts, while the proteins

CC are useful in preparing kits for the detection of soluble RANK, or

CC monitor RANK-related activity. The present sequence is a cDNA encoding

CC human RANK ligand (RANKL) protein.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

SO

Query Match 10.9%; Score 126; DB 22; Length 954;

Best Local Similarity 72.6%; Pred. No. 5.1e-30;

Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGGAGAGATATTGCTAAGATGCAATCCTGACGCTCAGCTCACTCATCTGTTA 524

DB 449 CATGGTTAGATCTGGCCAGAGAGACCTTGAAGCTCCTTCTCTATCTACACTA 508

QY 525 TTATATACCATCATATATCCATGAGGCT--CATAAACGAGTCTTCTTGTGAACATG 582

DB 509 TTATATGCCACCGACATCCCATCTGTTCCATTAAGTAGTCTGCTTGTGTCATG 568

QY 583 ACCAAGATTGGGCAACAGCTCTCCACATGACTTTCAGCAGGAAACTAAGATCA--- 639

DB 569 ATCGGGGTGGGCCCAAGATCTCCAAACATGACTTTAGCAATGGAATAATGTTAATC 628

QY 640 ---AAGCATTTATTAACCGGAATGCCCATTTGCTTCGACATGCGCTAACCCTGACAG 696

DB 629 AGGATGGCTTTTATTAATGCTATGCTCAACATTTGCTTTCGACATCATGAACCTCAGAG 688

QY 697 GCCTAAGCTGTCAGAGACCTTCAGCTA 722

DB 689 ACCTAGCTACAGAGATATCTTCACACTA 714

RESULT 7

AAD08715

ID AAD08715 standard; cDNA; 954 BP.

XX AAD08715;

AC AAD08715;

XX 04-SEP-2001 (first entry)

DT

XX Human receptor activator of NF-chi B ligand (huRANKL) cDNA.

DE

XX Human: receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF;

KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response;

KW chromosome 18q22.1; huRANKL; chromosome 13q14; Transmembrane protein; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT 1.954

FT CDS /tag= a

FT /product= "Human RANKL protein"

XX US6242213-B1.

PD 05-JUN-2001.

XX 22-DEC-1997; 97US-0995659.

XX 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0077181.

PR 14-OCT-1997; 97US-0064671.

XX (IMNV) IMMUNEX CORP.

PA Anderson DM;

XX WPI: 2001-407216/43.

DR P-PSDB; AAE04426.

XX New DNA molecules, useful for producing ligands (which are useful for

PT regulating immune response and in screening for inhibitors of NF-chi B

PT receptor activator) of the receptor activator of NF-chi B (RANK)

Query Match	10 98:	Score 126:	DB 24:	Length 1945:
Best Local Similarity	72.68:	Pred. No. 7.7e-30:		
Matches 193:	Conservative 0:	Mismatches 65:	Indels 8:	Gaps 2:
465	CAGGAGAGATATTGCTTAAGCAATGCAATCTGACGCTCAGCCTTGCACTCATCTTGTGA	524		
DB	324	CATGCTTAAGATCTGGCCAAAGAGCAAGAGCTTGAACTCTTGCTTGGCTCATCTCATACTA	383	
525	TTAATTAACATCAATATCCCATGAGGCT - CATAAAGAGAGCTTTTCTTGTGAACATG	582		

Dd		384	TTAATGGCACCAGCATGCCATCTCGTTCGCATTAAATGATGCTGTCTCCCTTGTTGACATG	443
OY		583	ACCAAGAATTGGGCAAACGTCCTCCAAATGACTTTTCAGCAAGSAAAACCTAAGAGTCA---	639
Dd		444	ATCGGGGTTGGGCCCAAGATCTCCAACTGACTTTTAGCAATGGAAAACTAAATAGTTAATC	503
OY		640	---AAGGATTTATTACCGGAATGGCCACAATTTGCTCGTGCATCGCGTAACCTCAGCAG	696
Dd		504	AGGATGGCTTTTATTACTGTATGCCAACACTTTGCTTTCGACATCATGAAACTTACGAG	563
OY		697	GCCTAACCTCTGACAGACCTTCAGCTA	722
Dd		564	ACCTAGCTACAGAGTATCTTCAACTA	589
RESULT 10				
ID	ABK12876		standard; cDNA; 2226 BP.	
XX	ABK12876;			
XX	18-JUN-2002	(first entry)		
Dt				
DE	cDNA encoding human TRANCE protein splice variant 1.			
XX				
KW	Human; tumour necrosis factor-related activation induced cytokine;			
KW	TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;			
KW	bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis			
KW	rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;			
KW	exostosis bursa; multiple osteocartilaginous exostosis; chondrocyte;			
KW	cartilage growth; skeletal growth; gene; ss.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	misc.feature	141..190		
FT	/tag= a			
FT	/note= "tumour necrosis factor (ligand) superfamily,			
FT	member 11 (TNFSF11), target region for antitumour			
FT	nucleic acid. Specifically claimed in claim 4"			
CDS	157..1110			
FT	/tag= b			
FT	/product= "Human TRANCE (tumour necrosis factor-related			
FT	activation induced cytokine) protein,			
FT	splice variant 1"			
WT				
PN	WO200216551-A2.			
PD	28-FEB-2002.			
PF	20-AUG-2001; 2001WO-US26101.			
PR	18-AUG-2000; 2000US-226197P.			
PA	(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.			
PI	Choi Y, Odgren PR, Marks SC:			
DR	WPT; 2002-304119/34.			
DR	P-PADB; AA078285.			
PT	Treating mammal having disorder characterised by abnormal			
PT	cartilage/skeletal growth such as dwarfism, acromegaly, by			
PT	administering tumour necrosis factor-related activation induced			
PT	cytokine-modulating agent to mammal -			
PS	Disclosure; Fig 1; 55pp; English.			
XX				
CC	The present invention relates to a new method of treating a mammal			
CC	having a disorder comprising insufficient or excessive cartilage or			
CC	skeletal growth. The method of the invention involves administering to			
CC	the mammal a tumour necrosis factor-related activation induced cytokine			

(TRANC) -modulating agent. The method is useful for treating a mammal having a disorder comprising insufficient or excessive cartilage or skeletal growth, where the disorder comprising insufficient cartilage or skeletal growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal discrepancies and bone or cartilage damage resulting from traumatic injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders comprising excessive cartilage or skeletal growth are selected from acromegaly, gigantism, exostosis, cartilage, exostosis bursata and multiple osteocartilaginous exostoses. The method is useful for inhibiting chondrocyte differentiation. The present nucleic acid sequence encodes the human TRANC protein, splice variant 1, of the invention. TRANC is a member of the tumour necrosis factor family and acts directly on cartilage-producing cells (chondrocytes).

Sequence 2226 BP; 656 A; 448 C; 505 G; 617 T; 0 other;

Query Match 10.9%; Score 126; DB 24; Length 2226;
Best Local Similarity 72.6%; Pred. No. 8.3e-30;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAGATTTTGGTAAAGATGCAATCCGACGCTTCACATCATCTGTGA 524
DB 605 CATGGTTAGATCTGGCCAAAGAGGACGCTGAGCTTGTCTCATCTCACTA 664
QY 525 TTATACCATCATATATCCCATGAGCT--CATAAACGAGCTTCTTCTTGGAACATG 582
DB 665 TTATGCGCCGACATCCCATCTGCTCCATTAAGTGCTGCTCTGTGATACGAG 724
QY 583 ACCAAGATTGGGCAAAAGCTCTCAACATGATCTTCAGCAAGCAAACTAAGAGTCA--- 639
DB 725 ATCGGGGTGGCCAAAGATCTCCCAACATGATCTTACGATGGAAGTAAATGTTAATC 784
QY 640 ---AAGCATTTATACCGGAATGCGACATTTGCTCTGCACATGCGTAACTCAGCAG 696
DB 785 AGGATGGCTTTTATACCTGTATGCAACATTTGCTTTCGACATCATGAAGTCAAGAG 844
QY 697 GCCTAACTCTGCAGACCTTCAGCTA 722
DB 845 ACCTAGCTACAGATATCTTCACTA 870

RESULT 11
AAZ99964
ID AAZ99964 standard; DNA; 2271 BP.

AC AAZ99964;

DT 25-JUL-2000 (first entry)

XX DNA encoding a human osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
XX tumour necrosis factor receptor; type II transmembrane protein;
XX osteoclast differentiation; CSF-1; osteoclast activator;
XX Immune response; osteoporosis; bone resorption; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 185..1138
XX FT /*tag= a

FT /*product= "osteoprotegerin ligand"

XX MO200015807-AL.

XX 23-MAR-2000.

XX 13-SEP-1999; 99WO-DK00481.

XX 15-SEP-1998; 98DK-0001164.

XX 02-OCT-1998; 98US-0102896.

XX (MEB1-) M & E BIOTECH AS.

XX Halkier T, Haaning J;
XX WPI: 2000-271444/23.
XX P-PSDB; AAY84417.
XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX to treat, prevent and ameliorate osteoporosis -
XX Disclosure; Page 75-77; 110pp; English.

XX The present sequence encodes a human osteoprotegerin ligand (OPGL).
XX Osteoprotegerin is a secreted member of the tumour necrosis factor
XX receptor family, which blocks osteoclastogenesis in a dose dependent
XX manner. The OPGL protein is synthesised as a type II transmembrane
XX protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX is a potent osteoclast differentiation factor when combined with CSF-1.
XX It is not capable of inducing osteoclast differentiation in the absence
XX of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX specification describes a method for the in vivo down-regulation of
XX OPGL activity in an animal. The method comprises using at least one OPGL
XX polypeptide or subsequence, and/or at least one OPGL analogue to induce
XX an immune response in the animal. The method and OPGL polypeptide are
XX useful for treating, preventing and ameliorating osteoporosis or other
XX diseases or conditions characterised by excessive bone resorption.

Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other;

Query Match 10.9%; Score 126; DB 21; Length 2271;
Best Local Similarity 72.6%; Pred. No. 8.4e-30;
Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 465 CAGAGAGATTTTGGTAAAGATGCAATCCGACGCTTCACATCATCTGTGA 524
DB 633 CATGGTTAGATCTGGCCAAAGAGGACGCTGAGCTTGTCTCATCTCACTA 692
QY 525 TTATACCATCATATATCCCATGAGCT--CATAAACGAGCTTCTTCTTGGAACATG 582
DB 693 TTATGCGCCGACATCCCATCTGCTCCATTAAGTGAAGTCTGCTGTGATACG 752
QY 583 ACCAAGATTGGGCAAAAGCTCTCAACATGATCTTCAGCAAGCAAACTAAGAGTCA--- 639
DB 753 ATCGGGGTGGCCAAAGATCTCCCAACATGATCTTACGATGGAAGTAAATGTTAATC 812
QY 640 ---AAGCATTTATACCGGAATGCGACATTTGCTCTGCACATGCGTAACTCAGCAG 696
DB 813 AGGATGGCTTTTATACCTGTATGCAACATTTGCTTTCGACATCATGAAGTCAAGAG 872
QY 697 GCCTAACTCTGCAGACCTTCAGCTA 722
DB 873 ACCTAGCTACAGATATCTTCACTA 898

RESULT 12

AAV70285
ID AAV70285 standard; DNA; 2274 BP.

AC AAV70285;

DT 11-FEB-1999 (first entry)

XX Human osteoprotegerin binding protein from the pcDNA/huopbpl.1insert.

XX Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
XX osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
XX hypercalcaemia; osteoclast differentiation and activation receptor;
XX Paget's disease; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 185..1138
XX FT /*tag= a

Db 754 CATGGTTAGATCTGGCCAGAGAGACGCTTAACCTCGCCTTTGGCTCATCTCACTA 813
 QY 525 TTAATACCATCAATATCCCATGAGGCT--CATAAACGAGCTCTTCTTCTTGGAAACATG 582
 Db 814 TTAAAGCCACCCAGATCCCATCTGCTTCCCATTAAGTGAAGTCTGCTCTGGTACCATG 873
 QY 583 ACCAGATTGGGCAACGCTCCACATGACTTTGACGCAAGGAAACTAAGTCA--- 639
 Db 874 ATCGGGGTTGGCCCAAGATCTCCACATGACTTTAGCAATGGAACATAATGATTATC 933
 QY 640 ---AAGCATTTATTAACCGGAATGCGACATTTGCTCTGACATCCGTAACCTCAGCAG 696
 Db 934 AGGATGGCTTTTATTAACCTGTATGCCAACAATTTGCTTGGACATCAATGAACCTTCAGAG 993
 QY 697 GCCTAATCTCTGACGAGACCTTCAGCTA 722
 Db 994 ACCTAGCTACAGAGTATCTTCAACTA 1019

RESULT 14

AA80223 standard; cDNA: 1823 BP.

AA80223;

17-AUG-1999 (first entry)

Human TRANCE encoding cDNA.

TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;

TNF-related activation induced cytokine; immune response; cancer;

autoimmune disease; HIV; hypersensitivity; allergen; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 1..738

/*tag= a

14-DEC-1998; 98WO-US26486.

11-DEC-1998; 98US-0989479.

12-DEC-1997; 97US-0989479.

03-MAR-1998; 98US-0034099.

(UVRQ) UNIV ROCKEFELLER.

Choi Y, Josien R, Steinman R, Won B;

WPI; 1999-385609/32.

P-PSDB; AAY17873.

TNF like proteins for treating autoimmunity and cancer

Claim 1; Fig 1; 164pp; English.

The present sequence encodes human TNF-related activation induced
 CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
 CC variants, fragments, derivatives or analogues may be used as modulators
 CC of immune response in a mammal comprising human and/or murine TRANCE.
 CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
 CC Agonists and antagonists of TRANCE, can be used to modulate immune
 CC response by increasing or decreasing the life span of mature dendritic
 CC cells and increasing or decreasing T cell activation. These techniques
 CC are especially useful for treating immune system related conditions such
 CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
 CC The TRANCE polypeptides can be used to increase the viability of
 CC dendritic cells in vivo or in vitro, especially when used in conjunction

CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
 CC CD40L or TNF-alpha).

SO Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

Query Match 10.6%; Score 122.8; DB 20; Length 1823;

Best Local Similarity 71.8%; Pred. No. 8; le-29;

Matches 191; Conservative 0; Mismatches 67; Indels 8; Gaps 2;

QY 465 CAGAGAGATTTTGCTAAGATGCAATCCAGAGCTCAGCCTTCAACTCATCTGTTA 524
 Db 233 CATGGTTAGATCTGGCCAGAGAGACGCTTGAAGCTTACGCTTCTCATCTCACTA 292
 QY 525 TTAATACCATCAATATCCCATGAGGCT--CATAAACGAGCTCTTCTTGGAAACATG 582
 Db 293 TTAAAGCCACCCAGATCCCATCTGCTTCCCATTAAGTGAAGTCTGTCCTTGTGCCATG 352
 QY 583 ACCAAGATTGGGCAACGCTCCACATGACTTTGACGCAAGGAAACTAAGTCA--- 639
 Db 353 ATCGGGGTTGGCCCAAGATCTCCACATGACTTTTGAACAATGAAACTAAGTTAATC 412
 QY 640 ---AAGCATTTATTAACCGGAATGCGACATTTGCTCTGACATCCGTAACCTCAGCAG 696
 Db 413 AGGATGGCTTTTATTAACCTGTATGCCAACAATTTGCTTGGACATCAATGAACCTTCAGAG 472
 QY 697 GCCTAATCTCTGACGAGACCTTCAGCTA 722
 Db 473 ACCTAGCTACAGAGTATCTTCAACTA 498

RESULT 15

AA86481 standard; cDNA: 957 BP.

AA86481;

29-JUN-2001 (first entry)

Rat osteoclast differentiation factor, ODF, coding sequence.

Rat; osteoclast formation inducer; vaccine; gene therapy;

Osteoclast Differentiation Factor; bone; ss.

Rattus sp.

Key Location/Qualifiers

CDS 1..957

/*tag= a

/product= "Rat ODF"

29-SEP-2000; 2000MO-AU01202.

29-SEP-1999; 99AU-0003147.

(UYWA-) UNIV WESTERN AUSTRALIA.

Xu J, Zheng M;

WPI; 2001-335526/35.

P-PSDB; AAB82092.

Novel nucleic acid encoding rat osteoclast differentiation factor
 useful for modulating activity of a cell, e.g., cell proliferation,
 cell differentiation and cell viability -

Claim 1; Fig 1; 81pp; English.

The present sequence is the coding sequence for rat Osteoclast
 Differentiation Factor (ODF). ODF is thought to be directly involved in

CC the differentiation of monocytes/macrophages into osteoclasts.
CC Osteoclasts promote dissolution of the bone matrix and solubilisation of
CC bone salts. The present sequence is useful in gene therapy, and as
CC hybridisation probes or primers. ODF protein is useful for modulating the
CC activity of cells, e.g., cell proliferation, cell differentiation and
CC cell viability, as immunogens to generate anti-rat ODF antibodies, and
CC as vaccines. Anti-rat ODF antibodies are useful in assay methods for
CC quantifying ODF polypeptides.
XX

SQ Sequence 957 BP; 230 A; 260 C; 256 G; 211 T; 0 other:

Query Match

Best Local Similarity 8.8%; Score 102; DB 22; Length 957;

Matches 169; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

QY 488 GGCATCTGAGCGCTGACCTTCACATCATCTGTATTATACCATATCCCATGA 547
DB 475 GGCATGCTGAGCGCTGAGCGCTTGTCTACCTCACATCATGCTGCCGACATCCCATCG 534
QY 548 GG--CTCATAAACGAGTCTTCTTCTTGGAACATGACCAAGATTGGCAAGCTCTCC 605
DB 535 GGTCCCATAAAGTCAGTGTCTCTTGTGACCATGATCGAGGCTGGCCAGATCTCT 594
QY 606 AACATGACTTTCGCAACGAGAAACTAAGAGTCA-----AAGCATTTATTACCGGAT 659
DB 595 AACATGACGTTAAGCAACGAGAAACTAAGGTTAACCAGATGGCTTCTATTACCTGTAC 654
QY 660 GCCGACATTTGCTCTGACATGCGGTAACTCAGACAGGCTTAACCTGACAGACCTTCAG 719
DB 655 GCCAACATTTGCTTCAAGCATCATGAAACCTCAAGGAGCGTACCTGGCGACTATCTTCAG 714
QY 720 CT 721
DB 715 CT 716

Search completed: December 8, 2002, 17:26:08
Job time : 341.592 secs

1
2
3
4

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 16:41:40 ; Search time 2486.23 Seconds
(without alignments)
13590.225 Million cell updates/sec

Title: US-09-880-457-1
Perfect score: 1161
Sequence: 1 aaagaaggaataatcaaga.....taataaaggaaggaataatgc 1161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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2:  gb_hcg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_or:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_higo_hum:*
40: em_higo_mus:*
41: em_higo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.4	40.3	165707	2 AC104794	AC104794 Homo sapi
2	467.4	40.3	190748	9 AC010969	AC010969 Homo sapi
3	268	23.1	1186	6 AX358828	AX358828 Sequence
4	268	23.1	1186	6 AX362321	AX362321 Sequence
5	204	17.6	157250	2 AC027264	AC027264 Homo sapi
6	126	10.9	954	6 AB064268	AB064268 Homo sapi
7	126	10.9	954	9 AB061227	AB061227 Homo sapi
8	126	10.9	930	9 AB037599	AB037599 Homo sapi
9	126	10.9	954	6 AB037599	AB037599 Homo sapi
10	126	10.9	954	6 AB037599	AB037599 Homo sapi
11	126	10.9	954	6 AB037599	AB037599 Homo sapi
12	126	10.9	954	6 AB037599	AB037599 Homo sapi
13	126	10.9	954	6 AB037599	AB037599 Homo sapi
14	126	10.9	954	6 AB037599	AB037599 Homo sapi
15	126	10.9	954	6 AB037599	AB037599 Homo sapi
16	126	10.9	954	6 AB037599	AB037599 Homo sapi
17	126	10.9	954	6 AB037599	AB037599 Homo sapi
18	123.8	10.6	1823	9 AF013171	AF013171 Homo sapi
19	102	8.8	957	10 AF013171	AF013171 Homo sapi
20	97.8	8.4	113451	2 AC023297	AC023297 Homo sapi
21	97.8	8.4	200724	9 AL139382	AL139382 Human DNA
22	97.8	8.4	754	10 AB032772	AB032772 Mus muscu
23	97.8	8.4	864	10 AB032771	AB032771 Mus muscu
24	97.8	8.4	951	6 E34350	E34350 DNA and pro
25	97.8	8.4	951	6 E36388	E36388 Novel prote
26	97.8	8.4	951	10 AB008426	AB008426 Mus muscu
27	97.8	8.4	951	10 AB036798	AB036798 Mus muscu
28	97.8	8.4	1630	6 AR156433	AR156433 Sequence
29	97.8	8.4	1630	6 AR164147	AR164147 Sequence
30	97.8	8.4	1630	6 AX147987	AX147987 Sequence
31	97.8	8.4	1630	6 AX451897	AX451897 Sequence
32	97.8	8.4	2191	6 AR157058	AR157058 Sequence
33	97.8	8.4	2191	6 AX140162	AX140162 Sequence
34	97.8	8.4	2225	10 AF019048	AF019048 Mus muscu
35	97.8	8.4	2237	10 AF013170	AF013170 Mus muscu
36	97.8	8.4	2237	6 AR062119	AR062119 Sequence
37	97.8	8.4	2299	6 AF053713	AF053713 Mus muscu
38	94.4	8.1	522	6 AX232589	AX232589 Sequence
39	84.8	7.3	127812	2 AC094149	AC094149 Rattus no
40	81.6	7.0	2029	6 E34349	E34349 DNA and pro
41	81.6	7.0	2029	10 AB022036	AB022036 Mus muscu
42	81.6	7.0	276831	2 AC126690	AC126690 Mus muscu
43	53	4.6	7218	6 I66494	I66494 Sequence 14
44	49.6	4.3	185512	9 AC012454	AC012454 Homo sapi
45	48.4	4.2	185371	9 AC083795	AC083795 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
Homo sapiens chromosome 2 clone RP11-254F7, WORKING DRAFT SEQUENCE,
3 unordered pieces.
AC104794
AC104794.3 GI:20340520
VERSION
HTG: HTGS_PHASE1, HTGS_DRAFT, HTGS_ACTIVEFIN.
KEYWORDS
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 165707)
Walterston, R.H.
TITLE
The sequence of Homo sapiens clone

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 3 (bases 1 to 165707)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 COMMENT On Apr 30, 2002 this sequence version replaced gi:19339129.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 Project Information
 Center project name: H.NH0254F07

----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: plasmid; 100%
 Chemistry: Dye-Primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 162662 bases at least Q40
 Consensus quality: 163189 bases at least Q30
 Consensus quality: 164786 bases at least Q20
 Insert size: 9479; agarose-fp
 Insert size: 167795; sum-of-contrigs
 Quality coverage: 12.78 in Q20 bases; agarose-fp
 Quality coverage: 10.53 in Q20 bases; sum-of-contrigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 3 contrigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contrigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. -----

1 1112: contrig of 1112 bp in length
 * 1113 1212: gap of unknown length
 * 1213 76227: contrig of 75015 bp in length
 * 76228 76327: gap of unknown length
 * 76328 165707: contrig of 89380 bp in length.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="2"
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BASE COUNT 42887 a 42242 c 39083 g 41295 t 200 others
 ORIGIN

Query Match 40.3%; Score 467.4; DB 2; Length 165707;
 Best Local Similarity 99.8%; Pred. No. 5.3e-134;
 Matches 468; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAGAGATATTCACAGAGGCTTTTAAAGGACTATTTCCCAAGATGGCATGAG 60
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 Db 40150 AAAAGAGATATTCACAGAGGCTTTTAAAGGACTATTTCCCAAGATGGCATGAG 40209

QY 61 GGAAACCTGCAGGGCTAGTCTCTACCTCCAGCAGGACGACTAATTCCTGAGGGAT 120
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 Db 40210 GGAAACCTGCAGGGCTAGTCTCTACCTCCAGCAGGACGACTAATTCCTGAGGGAT 40269

QY 121 AAGACGCTGTTGGAGAGACATGAGGGAAGTTCTACAGAGAGCAGTGGCTTCA 180
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 Db 40270 AAGACGCTGTTGGAGAGACATGAGGGAAGTTCTACAGAGAGCAGTGGCTTCA 40329

QY 181 GGAACACCTCTGAGAGGCTGTGAGAGGTTGGGATATCAATACCTGCTCTCC 240
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 Db 40330 GGAACACCTCTGAGAGGCTGTGAGAGGTTGGGATATCAATACCTGCTCTCC 40389

QY 241 TTCCATCTTCCCAACCCACAGAGGGTTGTGTGGGCCCCACAGGCGCTCCGGGGA 300
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QY 301 GAGAGTGGAGAGAGGAGACCTGGAGGCGCAGTAGAAGTATCCACACAATCTTACAAG 360
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 Db 40450 GAGAGTGGAGAGAGGAGACCTGGAGGCGCAGTAGAAGTATCCACACAATCTTACAAG 40509

QY 361 CACCAGCATTTTGTGAGCATTTGGATTGTGACCAACAGTCAGCAAAAAACCTTG 420
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 Db 40510 CACCAGCATTTTGTGAGCATTTGGATTGTGACCAACAGTCAGCAAAAAACCTTG 40569

QY 421 CTCTGTGGAGGAGACATTTAGCAAGAAGGCAATGACACACAGA 469
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 Db 40570 CTCTGTGGAGGAGACATTTAGCAAGAAGGCAATGACACACAGA 40618

RESULT 2
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 LOCUS
 DEFINITION
 AC010969
 AC010969.11 GI:13677120
 VERSION
 HTG.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 190748)
 Sulston, J.E. and Waterston, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1097-1108 (1998)
 99063792
 9847074

REFERENCE
 2 (bases 1 to 190748)
 Sun, H., Abbott, A. and Le, T.P.
 The sequence of Homo sapiens BAC clone RP11-95D17
 Unpublished
 3 (bases 1 to 190748)
 Waterston, R.H.
 Direct Submission
 Submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 4 (bases 1 to 190748)
 Waterston, R.H.
 Direct Submission
 Submitted (19-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 5 (bases 1 to 190748)
 Waterston, R.H.
 Direct Submission
 Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 6 (bases 1 to 190748)
 Waterston, R.
 Direct Submission
 Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

On Apr 19, 2001 this sequence version replaced gi:11128441.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: MUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: saplens@wustl.edu

----- Summary Statistics

Center project name: H_NH0095D17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-521D12. Actual start of this clone is at base position 1 of RP11-95D17; actual end is at base position 190748 of RP11-95D17.

There are polymorphic base differences between RP11-95D17 and the redundant clone AC062035. Data from AC062035 was used to finish RP11-95D17.

Unresolved tandem repeat from base position 181200 to 187300. Size information from restriction digest suggests that the full repeat may not be represented

FEATURES

source

Location/Qualifiers
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repeat_region
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806..1114
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Query Match 40.3%; Score 467.4; DB 9; Length 190748;
 Best Local Similarity 99.8%; Pred. No. 5.4e-134;
 Matches 468; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAGAGATTAATTCAGAGAGGCTTTCTTAAGGACTATTTCCCAAGATGGGAATGGAG 60
 Db 175455 AAAAGAGATTAATTCAGAGAGGCTTTCTTAAGGACTATTTCCCAAGATGGGAATGGAG 175396
 QY 61 GGAAGCTGAGGAGGCTAGTGTCTACCTCCAGAGGAGGAGCACTAATTTCTGAGGGAT 120
 Db 175395 GGAAGCTGAGGAGGCTAGTGTCTACCTCCAGAGGAGGAGCACTAATTTCTGAGGGAT 175336
 QY 121 AAGAGCTGTGTCGAGAGACATGAGGAAAGTTCTACAGAGAGGAGCAGAGTGGGCTTCA 180
 Db 175335 AAGAGCTGTGTCGAGAGACATGAGGAAAGTTCTACAGAGAGGAGCAGAGTGGGCTTCA 175276
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 Db 175275 GGAACACCTGCTTGAAGAGGCTTGAAGAGTGGGAATCAATCTGACCTGCTTCC 175216
 QY 241 TTCATCTCTCCCCAACCCACAGAGGCTTGTGTGTGGCCCAAGGCGAGCCTCCCGGGGA 300
 Db 175215 TTCATCTCTCCCCAACCCACAGAGGCTTGTGTGTGGCCCAAGGCGAGCCTCCCGGGGA 175156
 QY 301 GAGAAGTGGAGAGAGACCTGGAGGGGCTAGAGGTATGACACAGATATCTACAGG 360
 Db 175155 GAGAAGTGGAGAGAGACCTGGAGGGGCTAGAGGTATGACACAGATATCTACAGG 175096
 QY 361 CACCAAGCATTTTGTGAGCATTTGGGATTTGTGACAAACAGTCAACAAAAAACCCTG 420
 Db 175095 CACCAAGCATTTTGTGAGCATTTGGGATTTGTGACAAACAGTCAACAAAAAACCCTG 175036
 QY 421 CTCGTGGAGGAGCAATCTAGCAAGGAGGCAATGACAAAGCAGGA 469
 Db 175035 CTCGTGGAGGAGCAATCTAGCAAGGAGGCAATGACAAAGCAGGA 174987

RESULT 3
 AX358828 1186 bp DNA linear PAT 13-FEB-2002
 LOCUS Sequence 81 from Patent WO0193983.
 DEFINITION AX358828
 ACCESSION AX358828
 VERSION AX358828.1 GI:18675315
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
 Watanabe,C.K. and Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0193983-A 81 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 314 a 285 c 299 g 288 t
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 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 430 AGAGTATTTCCTAAGATGGCAATCCGAGGCTAGCCTTCACTCATCTTGTATTAA 489
 QY 529 TACCATCAATATCCCATGAGGCTCATAAAGAGCTTTCTCTTGGAAACATGACCAAG 588
 Db 490 TACCATCAATATCCCATGAGGCTCATAAAGAGCTTTCTCTTGGAAACATGACCAAG 549
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 Db 550 ATTGGGCAAAAGCTCCACATGACTTTTCAGCAACGAAACCTAAGAGTCAAGGCAATT 609
 QY 649 ATTACGGGAATGCCGACATTTGCTCGACATGCGCTTAACCTCAGAGGCTTAACCTGCG 708
 Db 610 ATTACGGGAATGCCGACATTTGCTCGACATGCGCTTAACCTCAGAGGCTTAACCTGCG 669
 QY 709 AGGACCTTCAGCTATGCTGTAATTTGAG 736
 Db 670 AGGACCTTCAGCTATGCTGTAATTTGAG 697

RESULT 4
 AX362321 1186 bp DNA linear PAT 15-FEB-2002
 LOCUS Sequence 81 from Patent WO0208288.
 DEFINITION AX362321
 ACCESSION AX362321
 VERSION AX362321.1 GI:18694618
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
 Watanabe,C.K. and Wood,W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 81 31-JAN-2002;
 Genentech, Inc. (US)
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 Location/Qualifiers
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 /db_xref="taxon:9606"

BASE COUNT 314 a 285 c 299 g 288 t
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Query Match 23.1%; Score 268; DB 6; Length 1186;
 Best Local Similarity 100.0%; Pred. No. 5.9e-72;
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QY 469 AGAGTATTTCCTAAGATGGCAATCCGAGGCTAGCCTTCACTCATCTTGTATTAA 528
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QY 709 AGGACCTTCAGTATGCTGAATTTGAG 736
 DB 670 AGGACCTTCAGTATGCTGAATTTGAG 697
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 AC027264/c
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 DEFINITION Homo sapiens chromosome 2 clone RP11-164P8 map 2, WORKING DRAFT
 AC027264 157250 bp DNA linear HTG 24-AUG-2002
 SEQUENCE 21 unordered pieces.
 AC027264 GI:10567976
 HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 157250)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 2, clone RP11-164P8
 Unpublished
 2 (bases 1 to 157250)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G.,
 Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
 Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczkzy,J.,
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 Murphy,T., Meneus,L., Mihova,T., Miranda,C., Menga,V., Morrow,J.,
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 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testage,S., Theodore,J., Tirtrell,A., Travers,M., Trigillo,J.,
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 157250)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavsky,L.,
 Bouckgalter,B., Brown,A., Burkett,G., Campoliano,A., Castle,A.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
 Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
 Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glnde,S., Goyette,M.,
 Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
 Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Lacroque,K.,
 Lamazares,R., Landers,T., Lehoczkzy,J., Levine,R., Lieu,C., Liu,G.,
 Macdonald,P., Margulis,N., McCarthy,M., McEwan,P., McKernan,K.,
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 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 4, 2000 this sequence version replaced gi:17331634.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www.seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: 164.P.8
 Center clone name: 164.P.8
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 144198 bases at least Q40
 Consensus quality: 151395 bases at least Q30
 Consensus quality: 153976 bases at least Q20
 Insert size: 155000; agarose-fp
 Insert size: 155250; sum-of-contrigs
 Quality coverage: 4.1 in Q20 bases; agarose-fp
 Quality coverage: 4.1 in Q20 bases; sum-of-contrigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contrigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contrigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1
 901 1000: gap of 100 bp in length
 1001 2288: contrig of 1288 bp in length
 2289 2388: gap of 100 bp
 2389 3949: contrig of 1561 bp in length
 3950 4049: gap of 100 bp
 4050 6137: contrig of 2088 bp in length
 6138 6237: gap of 100 bp
 6238 8049: contrig of 1812 bp in length
 8050 8149: gap of 100 bp
 8150 12625: contrig of 4476 bp in length
 12626 12725: gap of 100 bp
 12726 15710: contrig of 2985 bp in length
 15711 15810: gap of 100 bp
 15811 19721: contrig of 3911 bp in length
 19722 19821: gap of 100 bp
 19822 24311: contrig of 4490 bp in length
 24312 24411: gap of 100 bp
 24412 32675: contrig of 8264 bp in length
 32676 32775: gap of 100 bp
 32776 40400: contrig of 7625 bp in length
 40401 40500: gap of 100 bp
 40501 47416: contrig of 6916 bp in length
 47417 47516: gap of 100 bp
 47517 56743: contrig of 9227 bp in length
 56744 56843: gap of 100 bp
 56844 64404: contrig of 7561 bp in length
 64405 64504: gap of 100 bp
 64505 71871: contrig of 7367 bp in length
 71872 71971: gap of 100 bp
 71972 82019: contrig of 10048 bp in length
 82020 82119: gap of 100 bp
 82120 107411: contrig of 25292 bp in length
 107412 107511: gap of 100 bp
 107512 116168: contrig of 8657 bp in length
 116169 116268: gap of 100 bp
 116269 128458: contrig of 12190 bp in length
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 146713 146812: gap of 100 bp
 146813 157250: contrig of 10438 bp in length.
 Location/Qualifiers
 1. 157250

FEATURES
 source


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RESULT 7
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LOCUS             Homo sapiens mRNA for hRANKL 2, complete cds.
DEFINITION        AB061227.1 GI:16610212
ACCESSION         AB061227.1
VERSION           AB061227.1
KEYWORDS          Homo sapiens cDNA to mRNA.
SOURCE            Homo sapiens
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE         1
AUTHORS           Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE             Human RANKL isoform
JOURNAL           2 (bases 1 to 911)
REFERENCE         2
AUTHORS           Ikeda,T. and Kuroyama,H.
TITLE             Direct Submission
JOURNAL           Submitted (02-MAY-2001) Tohru Ikeda, Graduate School, Tokyo Medical
                  and Dental University, Pathology and Immunology, 1-5-45 Yushima,
                  Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp,
                  Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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QY 465 CAGGAGAACTATTGCTAAGATGCAATCGTCAAGCTCAAGCTTCAACTATCTTGTGA 524
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DB 466 TTAATGCCACCGACATCCATCTGTTCCATTAAGTAGAGTGTCTCTTGGTACCATG 525
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DB 586 AGGATGGCTTTTATTATACGTAATGATGATGCTTTCGACATCATGAAACTTCAGAG 645
QY 697 GCCTAACTCTGCAGGACCTTCAGCTA 722
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DB 646 ACCTAGCTACAGAGTATCTTCAACTA 671

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ORGANISM          Homo sapiens
REFERENCE         1
AUTHORS           Nagai,M., Kyakumoto,S. and Sato,N.
TITLE             Cancer cells responsible for humoral hypercalcemia express mRNA
                  encoding a secreted form of ODF/TRANCE that induces osteoclast
                  formation
JOURNAL           Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)
REFERENCE         20175237
AUTHORS           Nagai,M., Kyakumoto,S. and Sato,N.
TITLE             Direct Submission
JOURNAL           Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University
                  School of Dentistry, Department of Biochemistry, 19-1 Uchimaru,
                  Morioka, Iwate 020-8505, Japan (E-mail:mgagai@iwate-med.ac.jp,
                  Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)
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DB 324 CATGGTTATCATCTGGCCAGAGAGAGCAAGCTGAAGCTTGAGCTTTCATCATCTCACTA 383
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QY 640 ---AAGGCATTATTATACCGGAATGCCGACATTTGCTCTGCACATCGGTAACCTCAGAG 696
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DB 504 AGGATGGCTTTTATTATACGTAATGATGATGCTTTCGACATCATGAAACTTCAGAG 563
QY 697 GCCTAACTCTGCAGGACCTTCAGCTA 722
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DB 564 ACCTAGCTACAGAGTATCTTCAACTA 589

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RESULT 8
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DEFINITION        AB037599.1 GI:6863047
ACCESSION         AB037599.1
VERSION           AB037599.1
KEYWORDS          Homo sapiens male tongue epithelial-like squamous cell carcinoma
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RESULT 9
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LOCUS             ARI56434
DEFINITION        Sequence 12 from patent US 6242213.
ACCESSION         ARI56434
VERSION           ARI56434.1
KEYWORDS          GI:15125138

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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 954)
AUTHORS Anderson, D.M.
TITLE Isolated DNA molecules encoding RANK-L
JOURNAL Patent: US 6242213-A 12 05-JUN-2001;
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DEFINITION ARI64148
ACCESSION ARI64148
VERSION ARI64148.1 GI:16235114
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 954)
AUTHORS Dougall, W.C. and Galibert, L.
TITLE Receptor activator of NF-kappa.B
JOURNAL Patent: US 6271349-A 12 07-AUG-2001;
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Best Local Similarity 72.6%; Pred. No. 1.3e-27;
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DEFINITION AX147989
ACCESSION AX147989
VERSION AX147989.1 GI:14346964
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 954)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Receptor activator of nf-kappa b
JOURNAL Patent: WO 0136637-A 12 25-MAY-2001;
Immunex Corporation (US)
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BASE COUNT 255 a 239 c 227 g 233 t
ORIGIN
Query Match 10.9%; Score 126; DB 6; Length 954;
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DB 689 ACCTAGCTACAGAGTATCTTCAACTA 714
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LOCUS Sequence 5 from Patent WO0224896. 954 bp DNA linear PAT 03-JUL-2002
DEFINITION

Accession	Version	KeyWords	Source	Organism	Reference Authors Title	Journal	Features	CDS	BASE COUNT	ORIGIN
AX451895	AX451895.1	GI:21698735	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Screening assays for agonists or antagonists of receptor activat or of nt-db			
					Dougall, W.C.		Patent: WO 0224896-A 5 28-MAR-2002; IMMUNEX CORPORATION (US)			
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					Best Local Similarity		72.6%; Pred. No. 1.3e-27;			
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					AB064270					
					LOCUS					
					AB064270					
					DEFINITION					
					Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear					
					factor kappa B ligand 2-2, complete cds.					
					AB064270					
					AB064270.1 GI:18143620					
					KEYWORDS					
					ORGANISM					
					Homo sapiens					
					Homo sapiens					
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
					Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
					Ikeda, T., Kuroyama, H. and Hirokawa, K.					
					1					
					Determination of human RANKL isoforms					
					2 (bases 1 to 972)					

AUTHORS		Ikeda,T. and Kuroyama,H.	
TITLE	Direct Submission	Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail: tohru.pth@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)	
JOURNAL			
FEATURES	source	location/Qualifiers	
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DEFINITION	Homo sapiens hRANKL 1 mRNA for receptor activator of nuclear factor		
ACCESSION	AB064269		
VERSION	AB064269.1		
KEYWORDS	GI:18143618		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Ikeda,T., Kuroyama,H. and Hirokawa,K.		
TITLE	Determination Of human RANKL isoforms		
JOURNAL	Unpublished		
REFERENCE	2 (Bases 1 to 1034)		
AUTHORS	Ikeda,T. and Kuroyama,H.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental		

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(E-mail: toru.pch2med.tmd.ac.jp, Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)

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LOCUS
DEFINITION Homo sapiens receptor activator of nuclear factor kappa B ligand
(RANKL) mRNA, complete cds.

ACCESSION
AF019047
AF019047.1 GI:2612921

KEYWORDS
SOURCE

ORGANISM
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 2201)
Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.,
Tometsko, M.E., Roux, M.C., Teepe, M.C., Dubose, R.F., Cosman, D. and
Galibert, L.

TITLE
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function

JOURNAL
NATURE 390 (6656), 175-179 (1997)

MEDLINE
98032977

PUBMED
9367155
REFERENCE
2 (bases 1 to 2201)

AUTHORS
Anderson, D.M., Billingsley, W., Dougall, W., Maraskovsky, E.,
Cosman, D., Dubose, R., and Galibert, L.
DIRECT SUBMISSION
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA

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Query Match 10.9%; Score 126; DB 9; Length 2201;
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Matches 193; Conservative 0; Mismatches 65; Indels 8; Gaps 2;

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